STIC-Biotech/ChemLib 79094

From: Portner, Ginny
Sent: Wednesday, October 30, 2002 3:18 PM
To: STIC-Biotech/ChemLib
Subject: priority search

Importance: High

Please search the sequences in Application 09/910,186 (1) against 08/123,975; 60146,192; 60/133,866; 60/133868; 60/133869; 60/133,865; 60133,873 and (2) 60/133,867. Thanks

Ginny Portner
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Room 7e13
Mail box 7e12
(703) 308-7543

Ginny,
None of the provisional cases have CRF's, so I could only compare (1) with (2).
Barb

RECEIVED
OCT 30 2002
STIC

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Phone:	NA Sequences:	STN:
Location:	AA Sequences:	DIALOG:
Date Picked Up: 11-7	Structures:	Questel/Orbit:
Date Completed: 11-7-02	Bibliographic:	DRLink:
Searcher Prep/Review:	Litigation:	Lexis/Nexis:
Clerical:	Full text:	Sequence Sys.:
Online time:	Patent Family:	WWW/Internet:
	Other:	Other (specify):

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O| |C  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-1.res made by bobryen on Thu 7 Nov 102 14:39:29-PST.


Query sequence being compared:US-09-910-186A-1 (1-1332)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-1 (1-1332) with:
          File : US08123975A.seq

 100-
    -
    -
    -
  50-
    -
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    -
  10-
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    -
   5-
    -
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    -
    -
    -
   0-
    ---------------------------------------------------------------------
    |    |    |    |    |    |    |    |    |    |    |
SCORE 0   146  291  437  583  728  874  1020 1165 1311
STDEV        -1             0

                        PARAMETERS

Similarity matrix       Unitary     K-tuple                      4
Mismatch penalty              1     Joining penalty             30
Gap penalty                5.00     Window size                500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                           1053           539          446.29

Times:                      CPU                     Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name / Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4 Sequence 4, Application U	1338	1311	1314	0.58	0
2. US-08-123-975A-1 Sequence 1, Application U	1338	1311	1314	0.58	0
**** 1 standard deviation below mean ****					
3. US-08-123-975A-6 Sequence 6, Application U	1351	538	704	-1.15	0

1. US-09-910-186A-1 (1-1332)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 1311 Optimized Score = 1314 Significance = 0.58
Residue Identity = 984 Matches = 1314 Mismatches = 13
Gaps = 5 Conservative Substitutions = 0

```
      X    10        20        30        40        50        60        70
      GAATTCGAAACGAYGCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
      X    10        20        30        40        50        60        70

          80        90       100       110       120       130       140
      AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTGCCTACGCTTCCAAAATCAACATCGGTTCTAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTGCCTACGCTTCCAAAATCAACATCGGTTCTAAA
          80        90       100       110       120       130       140

         150       160       170       180       190       200       210
      GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
         150       160       170       180       190       200       210

         220       230       240       250       260       270       280
      CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
         220       230       240       250       260       270       280

      290       300       310       320       330       340       350       360
      TACTTCAAACCATCTCTCTGGAACAATGAATACACCATCAACTCGCATCGAAAATCAATTCTGGTTGGAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      TACTTCAACTCCATCTCTCTGAACAATGAATACACCATCAACTCGCATGGAAAACAATTCTGGTTGGAAA
      290       300       310       320       330       340       350

         370       380       390       400       410       420       430
      GTATCTTCGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
360      370       380       390       400       410       420       430

         440       450       460       470       480       490       500
      AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
         440       450       460       470       480       490       500

      510       520       530       540       550       560       570
      CTGAATAACTCCAAAATCTACATCAACGGCGCTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      CTGAATAACTCCAAAATCTACATCAACGGCGCTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
         510       520       530       540       550       560       570

      580       590       600       610       620       630       640
      CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACATCTACCGCTACATCTGGATCAAATAC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACATCTACCGCTACATCTGGATCAAATAC
         580       590       600       610       620       630       640

650       660       670       680       690       700       710       720
TTCAATCTGTTCGACAAAGAACTGAACGAAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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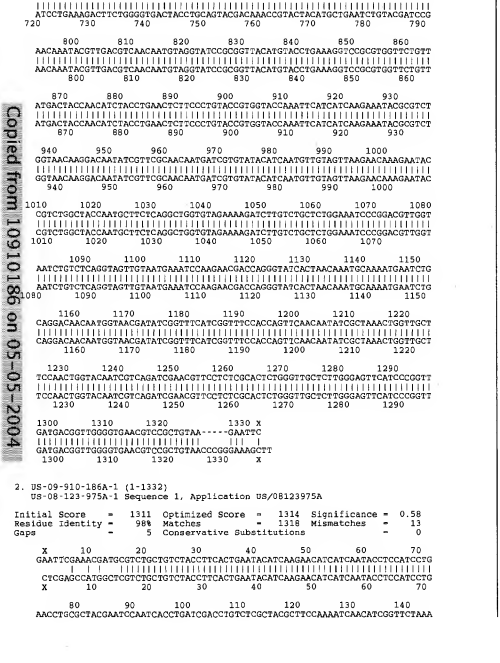
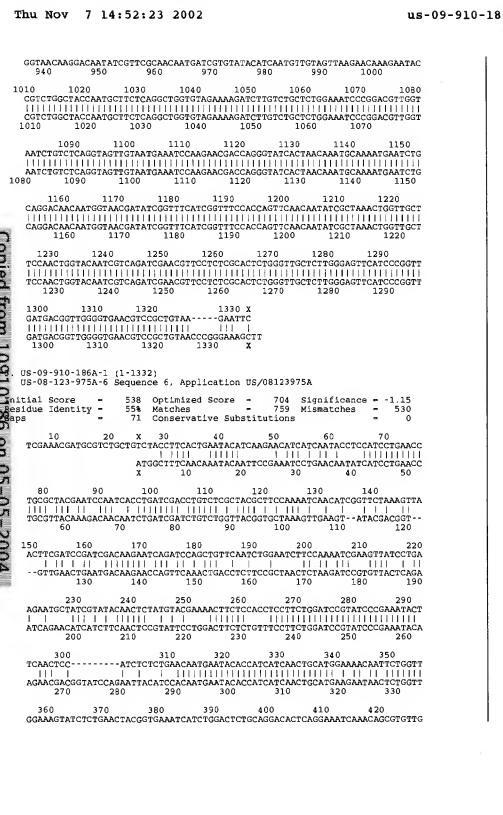


2. US-09-910-186A-1 (1-1332)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	1311	Optimized Score	= 1314	Significance = 0.58
Residue Identity	=	98%	Matches	= 1318	Mismatches = 13
Gaps	=	5	Conservative Substitutions	=	0



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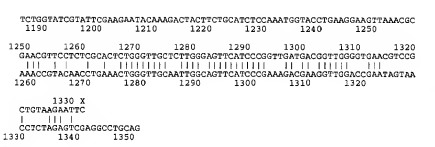

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Copied from 10914986 on 05/25/2004

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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-1-inv.res made by bobryen on Thu 7 Nov 102 14:39:50-PST.


Query sequence being compared:US-09-910-186A-1' (1-1332)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-1' (1-1332) with:
          File : US08123975A.seq
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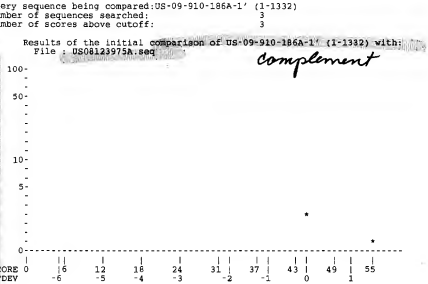
Complement




```
                              PARAMETERS

Similarity matrix          Unitary     K-tuple                        4
Mismatch penalty                 1     Joining penalty               30
Gap penalty                   5.00     Window size                  500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                          SEARCH STATISTICS

Scores:                       Mean       Median     Standard Deviation
                               47           45           6.35

Times:                         CPU                   Total Elapsed
                      00:00:00.00                   00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name      Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                    **** 1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    55   432   1.26    0
                    **** 0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    44   479  -0.47    0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    44   479  -0.47    0


1. US-09-910-186A-1' (1-1332)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     55  Optimized Score  =    432  Significance =  1.26
Residue Identity =    40%  Matches          =    515  Mismatches   =   658
Gaps             =     87  Conservative Substitutions              =     0

  80        90       100       110       120       130       140       150
  CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGCTGGAAACCGATC
                           ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                           x        10        20        30        40        50

      160       170       180       190       200       210       220
  AAACCGATACGGTTACCATCGTTGTCTGCAGATTCATTTTGCATTCTGTAATGATATCCCTGGTCGTTCTTG
  TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTCTAAAGTTGAAGTATACGACGGTGTTG
        60        70        80        90       100       110       120

      230       240       250       260       270       280       290
  GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
  AACTGAATGACAAGAAGCCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGCCGTTAC-
      130       140       150       160       170       180

      300       310       320       330       340       350       360
  CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTCTTCTTAACTACAACATTGATGTATACACCATCA
  TCAGAATCAGAA-CATCATCTTCAACTCCGTATTCCTGG--------ACTTCTCTGTTTCCTTCTCGATCC
      190       200       210       220       230       240

      370       380       390       400       410       420       430
  TTGTTCCGAACCATATTGTCCTTGTTA-CCAGACGGGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
  GTAATCCGAAATACAAGAAGTCAGGTATCCAGAATTACATCCACAAATGAATACACCATCATCAACTGCATGA
  250       260       270       280       290       300       310

  440       450       460       470       480       490       500
  GGAAGACTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGCGGACCTTCCAGGTACATGTAACCG
  AGAATAACTTCGGGTTGGAAGACTCCCATTCCGCGGTAACGTATCACTCGAC---TCTGATCGATATCAACG
320       330       340       350       360       370       380

      510       520       530       540       550       560       570
  CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
  GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
390       400       410       420       430       440       450

  580       590       600       610       620       630       640
  TACTGCAGGTAGTCACCCACAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGATT
  TTCTTC--GTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATA
  460       470       480       490       500       510       520

650       660       670       680       690       700       710
  TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
  CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
  530       540       550       560       570       580       590

      720       730       740       750       760       770
  TCAGGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
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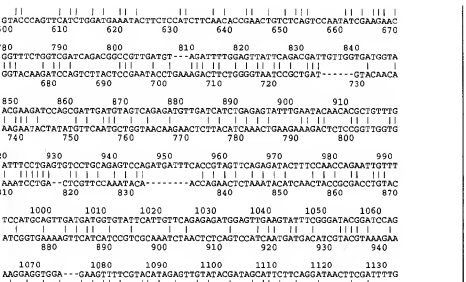

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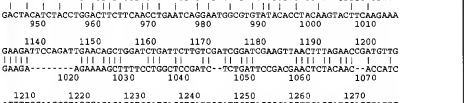
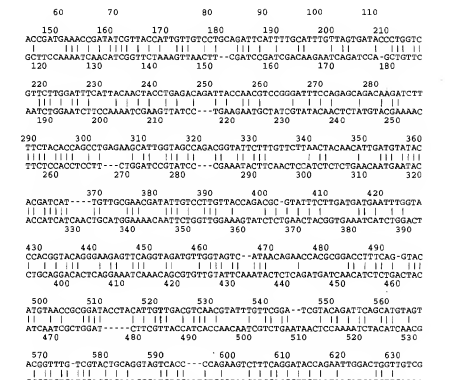
2. US-09-910-186A-1' (1-1332)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 44 Optimized Score = 479 Significance = -0.47
Residue Identity = 43% Matches = 584 Mismatches = 689
Gaps = 85 Conservative Substitutions = 0





Copied from 10910186 on 05-05-2004

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990     1000      1010      1020      1030      1040      1050
 TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
 |||  |||||| |||||| |||  |||  |||  |||  |||  |||  |||  |||   |||  |||
 GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
     960       970       980       990      1000      1010      1020

  1060      1070      1080      1090      1100      1110      1120
 GGATCCAGAAGGAGGTGGAGAAGTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
 | | |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
     1030      1040      1050      1060      1070      1080      1090

  1130      1140      1150      1160      1170      1180      1190
 CGATTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC-GAAGTTAACTTTAG
 | | |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAATCGCTAGCAGGACAACAATGG
     1100      1110      1120      1130      1140      1150      1160

  1200      1210      1220      1230      1240      1250
 AACCGAATGTTGATTT---TGGAAGCGTAGCGAGACCAGGTCGATCAGGTGATTGGATTCGTGAGCGCAGGT----
 | |||| | |||  |   |  |||  |||  |||  |||  |||  |||  |||  |   |  |||
 TAACGATATCGGTTCATCCGGTTCCACCAGTTCAACAATATCGCTAAACTGGTCGCTTCCAACTGGTACAA
     1170      1180      1190      1200      1210      1220      1230

  1260      1270      1280      1290      1300      1310      1320
 ---TCAGGATGGAGGTATTGATGATGTTC----TTGATGTATTCAGTGAAGGTAGACAGCAGACGCATCGTT
    |||| | | |||  |   |||  |  |||  | |||  |||  |||  |  |||  | | |  |
 TCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGG
 1240      1250      1260      1270      1280      1290      1300

  1330 X
 TCGAATTC
 | | ||
 TGAACGTCCGCTGTAACCCGGGAAAGCT
1310      1320      1330

US-09-910-186A-1' (1-1332)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    44  Optimized Score   =   479  Significance  =  -0.47
Residue Identity =   43%  Matches          =   584  Mismatches    =   689
Gaps             =    85  Consecutive Substitutions  =             =     0

          10        20        30        40        50        60        70
 GAATTCTTACAGCGGACGTTCACCCCAACGGTCATCAACCGGATGACTCCCAAGAGCAACCCAGAGTGCG
                   || |||||| |||| |||| |||| |||| |||| |||| |||| ||||
                   CTCGAGCCATGGCTCGTC-TGCTGTCTACCTCACTGAATACATCAAGAACATC
                   X        10        20        30        40        50

          80        90       100       110       120       130       140
 AGAGGACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
 | || | |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 ATCAATCCTCCATCTGGTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
      60        70                  80        90       100       110

     150       160       170       180       190       200       210
 ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
 | ||| | |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGATCAGATCCA-GCTGTTC
     120       130       140       150       160       170       180

     220       230       240       250       260       270       280
 GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
 | ||| | |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 AATCTGGAACTTCCAAATCGAAGTTATCC---TGAAGAATGCTATCGTAATACAACTCTATGTACGAAAAC
      190       200       210       220       230       240       250

290       300       310       320       330       340       350       360
 TTCTACACCAGCCTGGAGAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
 |||| |||| | ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTGAACAATGAATAC
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      260       270       280       290       300       310       320
 ACGATCAT---TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATTGGTA
 |||  |||   ||  |||  |||  |||  |||  |||  |||  | |||  |||  |||  |||
 ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
      330       340       350       360       370       380       390

 430       440       450       460       470       480       490
 CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
 | | |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  | |||
 CTGCAGGACCATCAGGAATCAAACCAGCGTTGTAATTCAAATACTCTCAGATGATCAAATACTCTCACTAC
      400       410       420       430       440       450       460

 500       510       520       530       540       550       560
 ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
 ||| |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 ATCAATCGCTGGAT-----CGTCGTTACCATCACCACACAATCGTCTGTAATAACTCCAAAATCTACATCAACG
      470       480       490       500       510       520       530

 570       580       590       600       610       620       630
 ACGGTTTG-TCGTACTGCAGGTAGTCACC----CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
 |||| |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 GCCGTCTGATCGACCAGAAACGGATCTCCAATCTGGGTATACAACCCACCCTTCTAAATAACATCATGTTCAAAC
      540       550       560       570       580       590       600

 640       650       660       670       680       690       700
 TACAGGTCTTTGATTTCTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
 ||| |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 TGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTCCAATCTGTTCGACAAAGACTGAACG
      610       620       630       640       650       660       670

 710       720       730       740       750       760       770
 TGAGTTCACGACAACCGTCCAGTTTGAACATGATGTTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
 ||| |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
      680       690       700       710       720       730       740

780       790       800       810       820       830       840       850
 GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGATTTATTCAGACGATTGTTGGTGATGGTAACG
 |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
      750       760       770       780       790       800       810

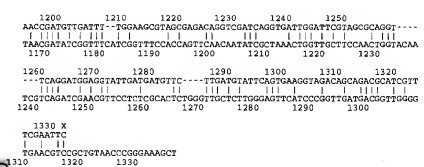
          860       870       880       890       900       910
 AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
 |||     |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGGCTGGTTCTGT-TATCACTACCAACATCTACC
          820       830       840       850       860       870       880

 920       930       940       950       960       970       980
 TGATTCCTGAGTGCCTCGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
 ||| |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
      890       900       910       920       930       940       950

990       1000      1010      1020      1030      1040      1050
 TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
 |||  |||||| |||||| |||  |||  |||  |||  |||  |||  |||  |||   |||  |||
 GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
     960       970       980       990      1000      1010      1020

  1060      1070      1080      1090      1100      1110      1120
 GGATCCAGAAGGAGGTGGAGAAGTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
 | | |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
      1030      1040      1050      1060      1070      1080      1090

  1130      1140      1150      1160      1170      1180      1190
 CGATTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
 | | |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
 AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAATCGCTAGCAGGACAACAATGG
     1100      1110      1120      1130      1140      1150      1160
```



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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-2.res made by bobryen on Thu 7 Nov 102 14:31:34-PST.


Query sequence being compared:US-09-910-186A-2 (1-437)
Number of sequences searched:                3
Number of scores above cutoff:               3

      Results of the initial comparison of US-09-910-186A-2 (1-437) with:
        File : US08123975A.pep

 100-
    -
    -
  50-
    -
    -
    -
    -
    -
  10-
    -
    -
   5-
    -
    -
    -
    -
    -
   0-----------------------------------------------------------------------
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
SCORE 0      46  |  92      138      184  |  231      277      323  |  369      415
STDEV        -1                         0                         1


                              PARAMETERS

Similarity matrix      PAM-150     K-tuple                          1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty                 20
Gap penalty               5.00     Window size                    437
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0


                           SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            262          181          132.08

Times:                      CPU                     Total Elapsed
                     00:00:00.00                  00:00:00.00

Number of residues:                        1704
Number of sequences searched:                 3
Number of scores above cutoff:                3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-3	Sequence 3, Application U	415	415	415	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-5	Sequence 5, Application U	439	193	273	-0.52	0
3. US-08-123-975A-2	Sequence 2, Application U	850	180	276	-0.62	0

```
1. US-09-910-186A-2 (1-437)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score   =  415  Optimized Score   =  415  Significance =  1.16
Residue Identity =  100%  Matches         =  415  Mismatches   =    0
Gaps            =    0  Conservative Substitutions            =    0

          10        20  X     30        40        50        60        70
   LLSTFTEYIKNIINTSILNRLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                                 ||||||||||||||||||||||||||||||||||||||||||||
                                 RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                                 X        10        20        30        40

      80        90        100       110       120       130       140
   YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
         60        70        80        90        100       110       120

    150       160       170       180       190       200       210
   NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
      130       140       150       160       170       180       190

   220       230       240       250       260       270       280       290
   ELNEKEIKDLTDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
    200       210       220       230       240       250       260

        300       310       320       330       340       350       360
   LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
270        280       290       300       310       320       330       340

      370       380       390       400       410       420       430
   VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
         350       360       370       380       390       400       410

    X
   RPL
   |||
   RPL
    X


2. US-09-910-186A-2 (1-437)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score   =  193  Optimized Score   =  273  Significance =  -0.52
Residue Identity =  38%  Matches         =  169  Mismatches   =   230
Gaps            =   17  Conservative Substitutions            =    26

       X 10        20        30        40        50        60        70
   MRLLSTPTEYIKNIINTSILNRLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNA
     |   |   |   ||||||  ||||| ::::: :   |   |||  |   |||  |
     TNKYNSELINNILNRLRYKDNWLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQWQN
     X         10        20        30        40        50        60
```

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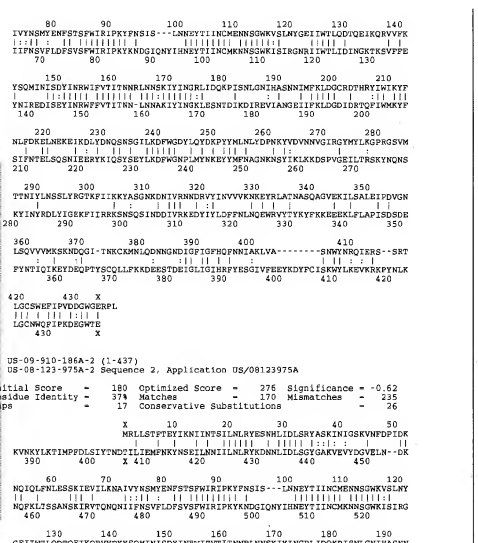

US-09-910-186A-2 (1-437)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score = 180 Optimized Score = 275 Significance = -0.62
Residue Identity = 37% Matches = 170 Mismatches = 235
Gaps = 17 Conservative Substitutions = 26

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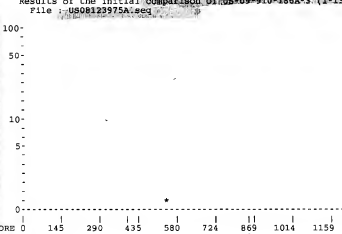
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3.res made by bobryen on Thu 7 Nov 102 14:40:15-PST.


Query sequence being compared:US-09-910-186A-3 (1-1323)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-3 (1-1323) with:
                File : USO8123975A.seq
```




```
                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                    SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                        1048         539                 442.25

Times:                   CPU                    Total Elapsed
                  00:00:00.00                 00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	1304	1305	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	1304	1305	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	538	704	-1.15	0

1. US-09-910-186A-3 (1-1323)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score    =  1304  Optimized Score  =  1305  Significance =  0.58
Residue Identity =    98% Matches          =  1309  Mismatches   =    14
Gaps             =     5  Conservative Substitutions             =     0

          X      10        20        30        40        50        60
          GAATTCGAAACGATGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
            10        20        30        40        50        60        70

          70        80        90       100       110       120       130
       ACCTGGGCTACGAATCCAATCACCTGATCGACCTGTCGTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       ACCTGGCTACGAATCCAATCACCTGATCGACCTGTCTGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
            80        90       100       110       120       130       140

         140       150       160       170       180       190       200
       TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
         150       160       170       180       190       200       210

       210       220       230       240       250       260       270       280
       TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
         220       230       240       250       260       270       280

               290       300       310       320       330       340       350
       ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
     290       300       310       320       330       340       350       360

               360       370       380       390       400       410       420
       TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
         370       380       390       400       410       420       430

               430       440       450       460       470       480       490
       AATACTCCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       AATACTCCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
         440       450       460       470       480       490       500

               510       520       530       540       550       560
       TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
         510       520       530       540       550       560       570

     570       580       590       600       610       620       630       640
       ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
     580       590       600       610       620       630       640

               650       660       670       680       690       700       710
       TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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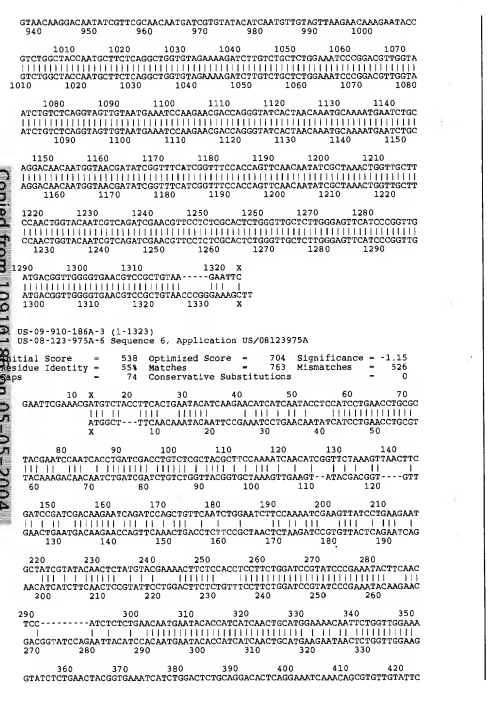
2. US-09-910-186A-3 (1-1323)
US-08-123-975A-1 Sequence 1, Application US/08123975A

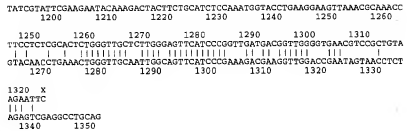
Initial Score = 1304 Optimized Score = 1305 Significance = 0.58
Residue Identity = 98% Matches = 1309 Mismatches = 14
Gaps = 5 Conservative Substitutions = 0

Copied from 10910186a on 05-05-2004



US-09-910-186A-3 (1-1323)
US-08-123-975-6 Sequence 6, Application US/08123975A

Initial Score = 538 Optimized Score = 704 Significance = -1.15
Residue Identity = 55% Matches = 763 Mismatches = 526
Gaps = 74 Conservative Substitutions = 0



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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3-inv.res made by bobryen on Thu 7 Nov 102 14:40:46-PST.


Query sequence being compared:US-09-910-186A-3' (1-1323)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-3' (1-1323) with:
          File : US08123975A.seq
```

complement

```
                        PARAMETERS

Similarity matrix          Unitary     K-tuple                    4
Mismatch penalty             1         Joining penalty           30
Gap penalty                  5.00      Window size              500
Gap size penalty             0.33
Cutoff score                 1
Randomization group          0

                      SEARCH STATISTICS

Scores:                    Mean        Median    Standard Deviation
                             47            45          6.35

Times:                      CPU                     Total Elapsed
                      00:00:00.00             00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Copied from 09/910,186 on 05/06/2004

```
                                                          Init.  Opt.
Sequence Name      Description                      Length Score Score  Sig. Frame
-------------------------------------------------------------------------------

                  **** 1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U     1351    55   429   1.26     0
                  **** 0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U     1338    44   475  -0.47     0
  3. US-08-123-975A-1 Sequence 1, Application U     1338    44   475  -0.47     0


1. US-09-910-186A-3' (1-1323)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     55  Optimized Score  =   429  Significance =  1.26
Residue Identity =    40%  Matches          =   518  Mismatches   =   663
Gaps             =     89  Conservative Substitutions            =     0

    80        90       100       110       120       130       140       150
  CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                                                    ||| | | | | | | | | | |
                                  ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                                  X        10        20        30        40        50

           160       170       180       190       200       210       220
  AAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTCGTTCTTG
          | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TGCGTTACAAAGACAACAATCTGATCGATCTGCTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

           230       240       250       260       270       280       290
  GATTTCATTACAACTACCTGAGACAGATACCAACGTCCGGATTTCCAGACGCAGACAAGATCTTTCTACA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
          130       140       150       160       170       180

           300       310       320       330       340       350       360
  CCAGCCTGAGAAGATTGGTAGCCACGAGGTATTCTTTGTTCCTAACTACAACATTGATGTATACACGATCA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TCAGAATCAGAA-CATCATCTTCAACTCCGTATTCCTGG---------ACTTCTCTGTTTCCTTCTGGATCC
          190       200       210       220       230       240

           370       380       390       400       410       420       430
  TTGTTGCGAACGATATTGTCCTTGTTA-CCAAGCGCGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  GTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACCATCATCCAACTGCATGA
          250       260       270       280       290       300       310

  440       450       460       470       480       490       500
  GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCAGCGGGACCTTTCAGGTACATGTAACCG
          | | | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  AGAATAACTCTGGTTGGAAGATCTCCCATCCGCGGTAACCGTATCATCGTCGAC---TCTGATCGAATATCAACG
320       330       340       350       360       370       380

          510       520       530       540       550       560       570
  CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAACGCTGC
390       400       410       420       430       440       450

  580       590       600       610       620       630       640
  TACTGCAGGTAGTCACCCCAGAAGTCTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGAAT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TTCTTC--GTTACCATCACCAATAACTGAACAATGCTAAAATCTACATCACGGTAACTGGAATCTAATA
          460       470       480       490       500       510       520

650       660       670       680       690       700       710
  TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
          | | | | | |       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
          530       540       550       560       570       580       590

               720       730       740       750       760               770
  TCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
```

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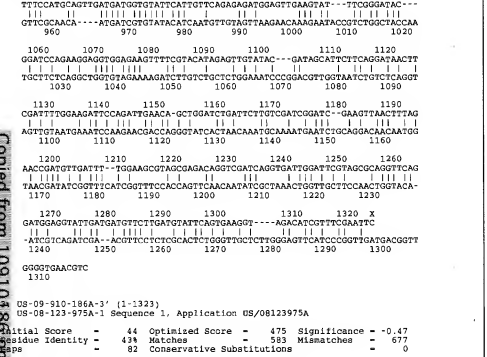
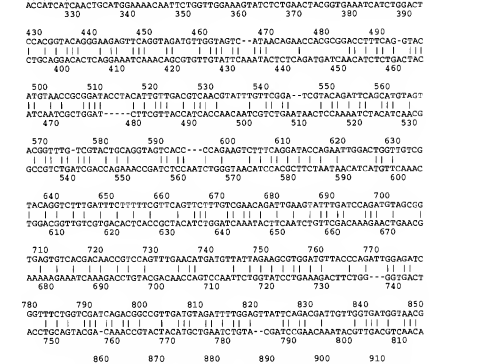
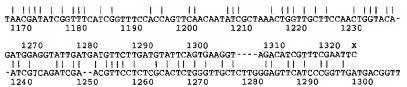
2 US-09-910-186A-3' (1-1323)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	44	Optimized Score	= 475	Significance = -0.47
Residue Identity	=	43%	Matches	= 583	Mismatches = 677
Gaps	=	82	Conservative Substitutions	=	0

Copied from 10910186a on 05-05-2004







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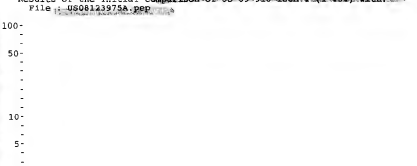
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-4.res made by bobryen on Thu 7 Nov 102 14:32:06-PST.


Query sequence being compared:US-09-910-186A-4 (1-434)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186a-4 (1-434) with:
            File : US08123975A.pep
```




```
                          PARAMETERS

Similarity matrix      PAM-150     K-tuple                        1
Threshold level of sim.    168
Mismatch penalty             1     Joining penalty               20
Gap penalty               5.00     Window size                  434
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                       SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            263          181          132.66

Times:                      CPU                     Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-3	Sequence 3, Application U	415	416	1.15	0
	**** 1 standard deviation above mean ****				
	**** 0 standard deviation from mean ****				
2. US-08-123-975A-5	Sequence 5, Application U	439	193	-0.53	0
3. US-08-123-975A-2	Sequence 2, Application U	850	180	-0.63	0

```
1. US-09-910-186A-4 (1-434)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =   416  Optimized Score  =   416  Significance =  1.15
Residue Identity =  100% Matches          =   415  Mismatches   =     0
Gaps             =     0  Conservative Substitutions =                 0

          10        20        30        40        50        60        70
MSPTFEYIKNIINTSILNLRYESNHLLDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                                  ||||||||||||||||||||||||||||||||||||||
                                  RYESNHLLDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                                  X        10        20        30        40        50

          80        90       100       110       120       130       140
NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
NSMYENFSTSFWIRIPKYFNSISLNNEYTIINGMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
          60        70        80        90       100       110       120

         150       160       170       180       190       200       210
ISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
         130       140       150       160       170       180       190

         220       230       240       250       260       270       280
LNKEKIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYWYLKGPRGSVWTTNIYL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
LNKEKIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYWYLKGPRGSVWTTNIYL
         200       210       220       230       240       250       260

         290       300       310       320       330       340       350
 NSSLYRGTKFTIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 NSSLYRGTKFTIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
270       280       290       300       310       320       330       340

         370       380       390       400       410       420       430
MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
         350       360       370       380       390       400       410

  X
  PL
  ||
  PL
  X

2. US-09-910-186A-4 (1-434)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   193  Optimized Score  =   273  Significance = -0.53
Residue Identity =  38% Matches           =   169  Mismatches   =   230
Gaps             =    17  Conservative Substitutions =                26

     X         10        20        30        40        50        60        70
MSTFPEYIKNIINTSILNLRYESNHLLDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
  |   |   | |  ||||||  | ||||| ::::: :   |   ||||  |   |||| |      |::
    FNKYNSELLNNILLNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIF
    X         10        20        30        40        50        60
```

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Copied from 10941986 on 05/20/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5.res made by bobryen on Thu 7 Nov 102 14:41:38-PST.


Query sequence being compared:US-09-910-186A-5 (1-1326)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-5 (1-1326) with:
          File = US08123975A.Seq
```



```
                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                    Mean      Median     Standard Deviation
                           1047         539                441.10

Times:                      CPU                    Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	1302	1307	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	1302	1307	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	538	704	-1.15	0

```
1. US-09-910-186A-5 (1-1326)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =  1302  Optimized Score  =  1307  Significance =  0.58
Residue Identity  =    98% Matches          =  1311  Mismatches   =    15
Gaps              =     5  Conservative Substitutions             =     0

        X   10        20        30        40        50        60
        GAATTCGAAACGATGGCCTCTACCTTCCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
        |   |         |         |         |         |         |         |
CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
        X  10        20        30        40        50        60        70

 70        80        90       100       110       120       130
 |         |         |         |         |         |         |
 ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
           80        90       100       110       120       130       140

140       150       160       170       180       190       200       210
TTAACTTCGATCCGATCGACAAGAAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
    150       160       170       180       190       200       210

          220       230       240       250       260       270       280
TGAAGAATGCTATCGTATACAACTCTATGTATGCAGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAAGAATGCTATCGTATACAACTCTATGTATGCAGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
    220       230       240       250       260       270       280

              290       300       310       320       330       340       350
ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATTGGAAAACAATTCTGGTTGGAAAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATTGGAAAACAATTCTGGTTGGAAAG
290       300       310       320       330       340       350       360

    360       370       380       390       400       410       420
TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
        370       380       390       400       410       420       430

430       440       450       460       470       480       490
AATACTCTCAGATGATCAACACTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATACTCTCAGATGATCAACACTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
    440       450       460       470       480       490       500

500       510       520       530       540       550       560       570
TGAATAACTCCAAAATCTACATCAACGGCCCTCTGATCGACCAGAAACCGAYCTCCAATCTGGGTAACATCC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAATAACTCCAAAATCTACATCAACGGCCCTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
    510       520       530       540       550       560       570

          580       590       600       610       620       630       640
ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
580       590       600       610       620       630       640

    650       660       670       680       690       700       710
TCAATCTCTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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2. US-09-910-186A-5 (1-1326)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	1302	Optimized Score	=	1307	Significance	= 0.58
Residue Identity	=	98%	Matches	=	1311	Mismatches	= 15
Gaps	=	5	Conservative Substitutions	=	0		

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US-09-910-186A-5 (1-1326)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 538 Optimized Score = 704 Significance = -1.15
Residue Identity = 55% Matches = 759 Mismatches = 530
Gaps = 71 Conservative Substitutions = 0

```
   TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAA
1190       1200       1210       1220       1230       1240       1250

     1250       1260       1270       1280       1290       1300       1310
   ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCT
   ||  |   |  |  ||||||| |||| ||||||||||   || || ||||||  |||     |  |
   ACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAGACGAAGGTTGGACCGAATAGTAACC
1260       1270       1280       1290       1300       1310       1320       1330

   1320     X
   GTAAGAATTC
      ||||  |
   TCTAGAGTCGAGGCCTGCAG
        1340       1350
```

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Created from 09910186a on 07.11.2002

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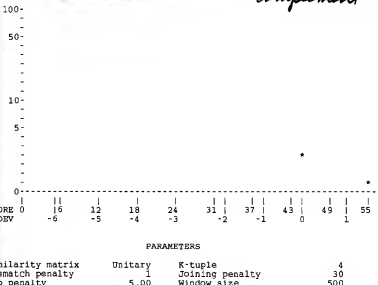
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5-inv.res made by bobryen on Thu 7 Nov 102 14:41:54-PST.


Query sequence being compared:US-09-910-186A-5' (1-1326)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-5' (1-1326) with:
          File : US08123975A.seq
```

complement




```
                        PARAMETERS

Similarity matrix          Unitary     K-tuple                    4
Mismatch penalty             1         Joining penalty           30
Gap penalty                 5.00       Window size              500
Gap size penalty            0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                    Mean        Median     Standard Deviation
                             47            45                   6.35

Times:                      CPU                   Total Elapsed
                     00:00:00.00                00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	55	430	1.26	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	44	478	-0.47	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	44	478	-0.47	0

```
1. US-09-910-186A-5' (1-1326)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =     55  Optimized Score  =    430  Significance =  1.26
Residue Identity  =     40% Matches          =    519  Mismatches   =   665
Gaps              =     89  Conservative Substitutions               =     0

  80        90       100       110       120       130       140       150
  CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTACGCAATATTGTTGAACTGGTGGAAACCGATG
                                 | | | | | | | | | | | | | | | | | | | | |
                                 ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                                 X         10        20        30        40        50

           160       170       180       190       200       210       220
  AAACCGATATCGTTACCATTCGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTCGTCTTG
    . | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TGCGTTACAAAGACAACAATCTGATCGATCGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

           230       240       250       260       270       280       290
  GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  AACTGAATGACAAGACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
          130       140       150       160       170       180

           300       310       320       330       340       350       360
  CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCCTTAACTACAACATTGATGTATACAGGATCA
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  ICAGAATCAGAA-CGTCATCTTCAACTCCGTATTCCTGG---------ACTTTCCTGTTTCCTTCGTGATCC
          190       200       210       220       230       240

  370       380       390       400       410       420       430
  TTGTTGCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  GTATCCCGAATACAAGAAACGACGGTATCCAGAATTACATCCACAATGGAATACCACATCATCCAACTGCATGA
  250       260       270       280       290       300       310

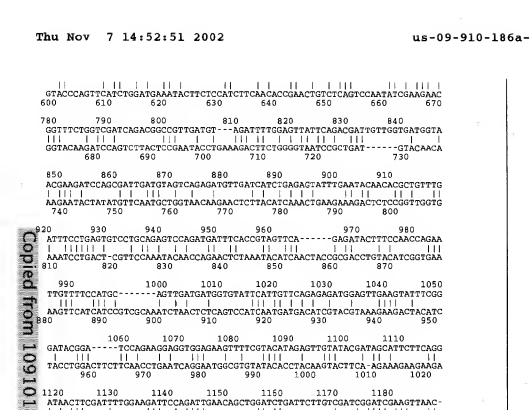
  440       450       460       470       480       490       500
  GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGCGACCTTTCAGGTACATGTAACCG
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  AGAATAACTCTGGTTGGGAGATCCCAATCCGCGGTAACCGTATCATCTGGAC---TCTGATCGATATCAAGG
320       330       340       350       360       370       380

    510       520       530       540       550       560       570
  CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCACGATGTAGTACGGTTTGTCG
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
390       400       410       420       430       440       450

  580       590       600       610       620       630       640
  TACTGCAGGTAGTCACCCCAGAAGTCTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCCTTGATT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TTCTTC--GTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATA
    460       470       480       490       500       510       520

650       660       670       680       690       700       710
TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
  |   | | | | | |      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
    530       540       550       560       570       580       590

        720       730       740       750       760       770
  TCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
```



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2. US-09-910-186A-5' (1-1326)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	44	Optimized Score	= 478	Significance = -0.47
Residue Identity	=	43%	Matches	= 582	Mismatches = 681
Gaps	=	78	Conservative Substitutions	=	0

Copied from 10910186 on 05-05-2004

```
990      1000      1010      1020      1030      1040      1050
  TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
        960       970       980       990      1000      1010      1020

  1060      1070      1080      1090      1100      1110      1120
  GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCGGAAATCCGGGACGTTGGTAATCTGTCTCAGGT
        1030      1040      1050      1060      1070      1080      1090

  1130      1140      1150      1160      1170      1180      1190
  CGATTTTGGAAACATTCCAGATTGAACA-GCTGGATCTGATTCTTTGTCGATCGGATC--GAAGTTAACTTTAG
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
        1100      1110      1120      1130      1140      1150      1160

  1200      1210      1220      1230      1240      1250      1260
  AACCGATGGTTGATTT--TGGAAGCGTAACGAGACAGGTCGATCAGGTGATTGGATTCGTAGCCGAGGTTCAG
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     TAACGATATCGGTTCATCGGTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
        1170      1180      1190      1200      1210      1220      1230

  1270      1280      1290      1300      1310      1320      X
  GATGGAGGTATTGATGATGTTCTGATGTATTCAGTGAAGGTAGAGGCCATCGTTTCGAATTC
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||
     -ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGAGTTCATCCCGGTTGATGACGGTT
        1240      1250      1260      1270      1280      1290      1300

  GGGGTGAACGT
  1310

US-09-910-186A-5' (1-1326)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    44  Optimized Score   =   478  Significance  = -0.47
Residue Identity =   43%  Matches           =   582  Mismatches    =   681
Gaps             =    78  Conservative Substitutions  =     .      =     0

        10        20        30        40        50        60        70
  GAATTCTTACAGCGGACGTTCACCCCAACGTCATCAACGGGATGAACTCCCAAGACAACCCAGAGTGCGG
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
        CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
           X       10        20        30        40        50

     80        90       100       110       120       130       140
  AGAGGAGCGTTCGATTCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
        60        70        80        90       100       110

    150       160       170       180       190       200       210
  ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     CTTCCAAAATCAACATCGGTTCTAAAGTTAACTT---CGATCCGACCGACAACAATCAGATCCA-GCTGTTC
       120       130       140       150       160       170       180

    220       230       240       250       260       270       280
  GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGCAAGATCTT
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     AATCTGCAATCTTCCAAAATCGAGTTATCC---TGAAGAATGCTATCGTATACAACTCTCATGTACCAAAAC
       190       200       210       220       230       240       250

    290       300       310       320       330       340       350       360
  TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
     TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
       260       270       280       290       300       310       320

              370       380       390       400       410       420
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ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
 |||||||    ||  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
          330       340       350       360       370       380       390

430       440       450       460       470       480       490
CCAGGGTACAGGGAAGAGTTCAGGTAGATGTTTGGTAGTC--ATAACAGAACCACGCGGACCTTCAG-GTAC
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
     400       410       420       430       440       450       460

 500       510       520       530       540       550       560
ATGTAACCGCGGATAACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
ATCATGGCTGGAT----CTTCGTTACCACTCACCAACAATCGTCTGAATGAACTCCTACAAAATCTACATCAACG
     470       480       490       500       510       520       530

 570       580       590       600       610       620       630
ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
GCCGTCTGATCGACCAGAAACGAATCTCCAATCTGGGTAACATCCAGCTTCTAATAACATCATGTCCAAACT
     540       550       560       570       580       590       600

 640       650       660       670       680       690       700
TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
TGGACGGTTGTCGTGACACTCACCGCTACATCCTGATGTCGACAAAGACTTCAATCTGTTCGACAAAGACAAGC
     610       620       630       640       650       660       670

 710       720       730       740       750       760       770
TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGTTGATCCTGAAAGACTTCTGG---GGTGACAT
     680       690       700       710       720       730       740

780       790       800       810       820       830       840       850
GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGATTATTCAGACGATTGTTGGTGATGGTAACG
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
     750       760       770       780       790       800       810

 860       870       880       890       900       910       920
AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
 |||     |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
          820       830       840       850       860       870       880

 930       940       950       960       970       980
TGATTTCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
 |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||
TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
     890       900       910       920       930       940       950

990      1000      1010      1020      1030      1040      1050
TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
   |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
   GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
      960       970       980       990      1000      1010      1020

 1060      1070      1080      1090      1100      1110      1120
 GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
    |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
    TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCGGAAATCCGGGACGTTGGTAATCTGTCTCAGGT
       1030      1040      1050      1060      1070      1080      1090

 1130      1140      1150      1160      1170      1180      1190
 CGATTTTGGAAACATTCCAGATTGAACA-GCTGGATCTGATTCTTTGTCGATCGGATC--GAAGTTAACTTTAG
    |||  |  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
    AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
       1100      1110      1120      1130      1140      1150      1160

 1200      1210      1220      1230      1240      1250      1260
 AACCGATGTTGATTT--TGGAAGCGTAACGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAG
```

```
TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
 1170       1180       1190       1200       1210       1220       1230

   1270       1280       1290       1300       1310       1320       X
GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGAGGCCA?CGTTTCGAATTC
-AICGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
 1240       1250       1260       1270       1280       1290       1300

GGGGTGAACGT
 1310
```

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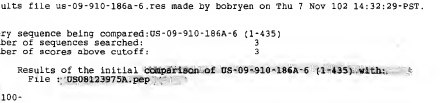
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-6.res made by bobryen on Thu 7 Nov 102 14:32:29-PST.


Query sequence being compared:US-09-910-186A-6 (1-435)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-6 (1-435) with:
          File : USOB123975A.pep
```




```
                                PARAMETERS

Similarity matrix          PAM-150      K-tuple                      1
Threshold level of sim.      16%
Mismatch penalty               1      Joining penalty             20
Gap penalty                 5.00      Window size                435
Gap size penalty            0.05
Cutoff score                   1
Randomization group            0

                            SEARCH STATISTICS

Scores:                      Mean       Median     Standard Deviation
                              263          181          132.66

Times:                        CPU                     Total Elapsed
                      00:00:00.00                     00:00:00.00

Number of residues:                        1704
Number of sequences searched:                 3
Number of scores above cutoff:                3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-3	Sequence 3, Application U	435	416	416	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-5	Sequence 5, Application U	439	193	273	-0.53	0
3. US-08-123-975A-2	Sequence 2, Application U	850	180	275	-0.63	0

```
1. US-09-910-186A-6 (1-435)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =   416  Optimized Score  =   416  Significance =  1.15
Residue Identity =   100% Matches          =   435  Mismatches   =     0
Gaps             =     0  Conservative Substitutions             =     0

          10        20        30        40        50        60        70
MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                                                                        |
                                                                        |
                                                                        |
```

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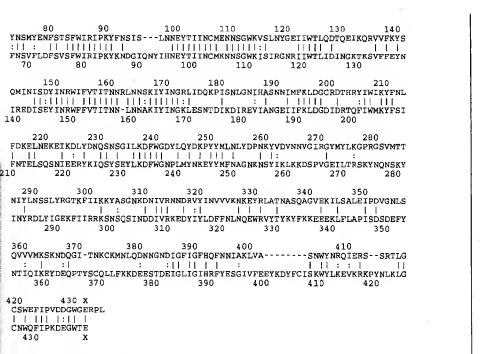

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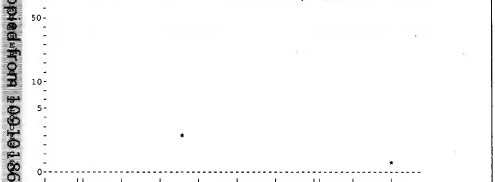
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7.res made by bobryen on Thu 7 Nov 102 14:42:16-PST.


Query sequence being compared:US-09-910-186A-7 (1-1341)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

        Results of the initial comparison of US-09-910-186A-7 (1-1341) with:
          File  US08123975A.seq
```




```
                              PARAMETERS

Similarity matrix       Unitary      K-tuple                    4
Mismatch penalty              1      Joining penalty           30
Gap penalty                5.00      Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            795           534                  454.37

Times:                      CPU                    Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	1320	1323	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	533	699	-0.58	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	533	699	-0.58	0

```
1. US-09-910-186A-7 (1-1341)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =  1320  Optimized Score  =  1323  Significance =  1.16
Residue Identity =    99% Matches          =  1323  Mismatches   =    12
Gaps             =     0  Conservative Substitutions =                  0

          X 10        20        30        40        50        60        70
 GAATTCACGATGGCCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGAC
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGAC
           X        10        20        30        40        50        60

          80        90       100       110       120       130       140
 AACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAG
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 AACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAG
    70        80        90       100       110       120       130

         150       160       170       180       190       200       210
 AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
140       150       160       170       180       190       200       210

  220       230       240       250       260       270       280
 TCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATTCGTATCCGSAAATACAAGAACGACGGTATCCAGAAT
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATTCGTATCCGSAAATACAAGAACGACGGTATCCAGAAT
          220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
 TACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
    290       300       310       320       330       340       350

          370       380       390       400       410       420       430
 AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGT
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGT
    360       370       380       390       400       410       420

  440       450       460       470       480       490       500
 GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
  430       440       450       460       470       480       490

    510       520       530       540       550       560       570
 TACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATC
500       510       520       530       540       550       560       570

  580       590       600       610       620       630       640
 ATCTTCAAACTGGACGGTGACATCGATGCTATACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 ATCTTCAAACTGGACGGTGACATCGATGCTATACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACC
          580       590       600       610       620       630       640

650       660       670       680       690       700       710       720
 GAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG
```

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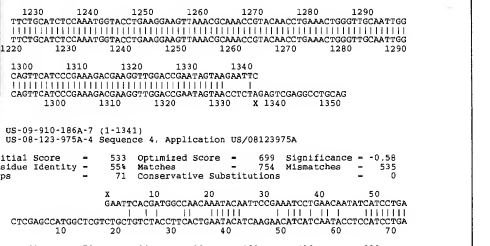
2. US-09-910-186A-7 (1-1341)
US-08-123-975A-4 Sequence 4. Application US/08123975A

Initial Score	=	533	Optimized Score	=	699	Significance	= -0.58
Residue Identity	=	554	Matches	=	754	Mismatches	= 535
Gaps		71	Conservative Substitutions				= 0



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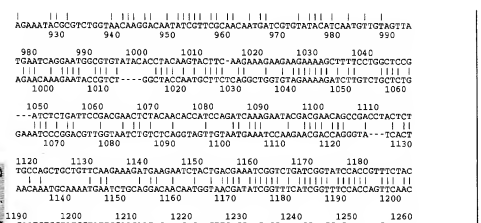
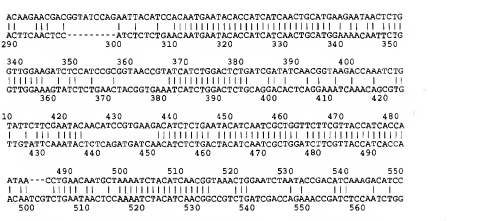
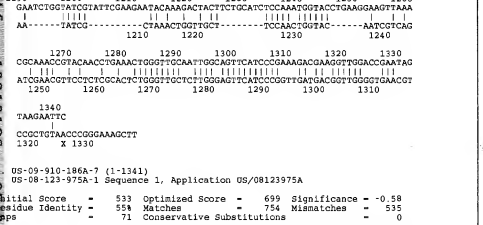
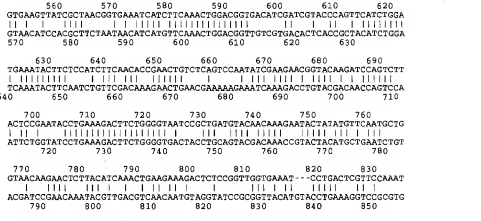
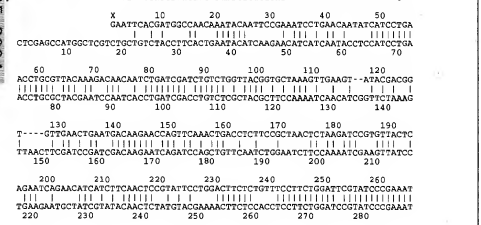
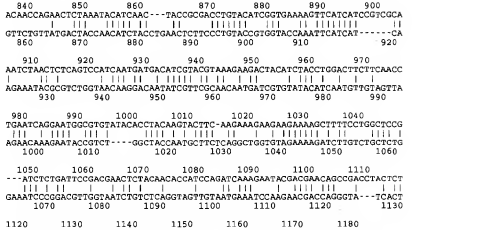






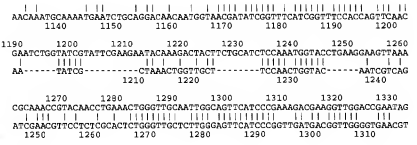






US-09-910-186A-7 (1-1341)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	533	Optimized Score	= 699	Significance = -0.58
Residue Identity	=	55%	Matches	= 754	Mismatches = 535
Gaps	=	71	Conservative Substitutions	=	0



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Copied from 10/916,186 on 05/13/2004

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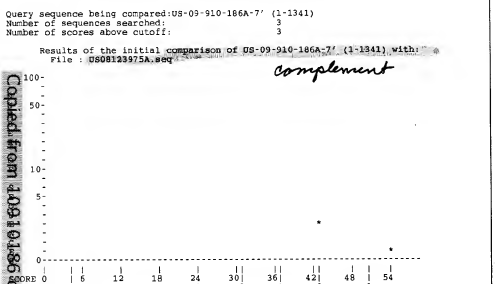
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7-inv.res made by bobryen on Thu 7 Nov 102 14:42:32-PST.


Query sequence being compared:US-09-910-186A-7' (1-1341)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-7' (1-1341) with:
          File : US08123975A.seq
```




```
                        PARAMETERS

Similarity matrix      Unitary     K-tuple                    4
Mismatch penalty             1     Joining penalty           30
Gap penalty               5.00     Window size              500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                     SEARCH STATISTICS

Scores:                    Mean      Median    Standard Deviation
                             46          44                  6.35

Times:                      CPU                    Total Elapsed
                     00:00:00.00                 00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	54	488	1.26	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	43	481	-0.47	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	43	481	-0.47	0

```
1. US-09-910-186A-7' (1-1341)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    54  Optimized Score   =   488  Significance =  1.26
Residue Identity =   43%  Matches           =   563  Mismatches   =   716
Gaps             =    90  Conservative Substitutions               =     0

                        X        10        20        30        40
                GAATTCTT--ACTATTCGGTCC--AACCTTCGTCTTTCGGGATGAACTGCCA
                |||| ||| |   |||| |||   |||  |||||||||||||||||||||||
    CTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAATCTGA
       10        20   X   30        40        50        60        70

    50        60        70        80        90       100       110
    ATTGCAACCCAGTTTCAGGTTGTACGGTTTGCGTTTA--ACTTCCTTCA--GGTACCATTTGGAGATGCAGA
    |  | | |  |  |||  ||  ||  ||||||||||  ||||  ||  ||  |||| |  | | |  |||
    TCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAGTTCA
      80        90       100       110       120       130       140

     120       130       140       150       160       170       180
    AGTAGTCTTTGTATTCTTCGAATACGATACCAGATTCGTAGAAACGGTGGATACCGATCAGACCGATTTCGT
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
    AACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCC
    150       160       170       180       190       200       210       220

    190       200       210       220       230       240       250
    CAGTAGATTCTTCATCTTCTTCTGAACAGCGCAGCTGGCAAGAGTAGGTCGGCTGTTCGTCGTATTCTTT-----
       |  |||  | ||||||  | ||  |  |  |  |  | | | |  |  |  |  |  |  |  |||  |
    TGGACTTCTCTGTTTCCTTCTGGATCCGTATCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACA
          230       240       250       260       270       280       290

                260       270       280       290       300       310
    ----------GATCTGGATGGTGTTGTAGAGTTCGTCGAATCAGAGATC-GGAGACGAGGAAAAGCTTTTCT
              |||  |  |  |||| |  | |  |  |||||  | ||  | |  |  |  |  |  |||
    ATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCCTCCATCCGCGGTAACGTTATCA
          300       310       320       330       340       350       360

     320       330       340       350       360                   370
    TCTTCTTTCTTGAAGTACTTGTAGGTGTATACACGCCATTCCTGATTCA--------GGTTGAAGAAGTCC
    |||  |||  |  |  |||  |  |  |  |  |  |  |  |  |  |        ||||||  ||
    TCTGGACTCTGATCGATATCAACGGTAAGACCAAACTGTATTCTCGAATACAACATCCGTGAAGAGATCT
       370       380       390       400       410       420       430

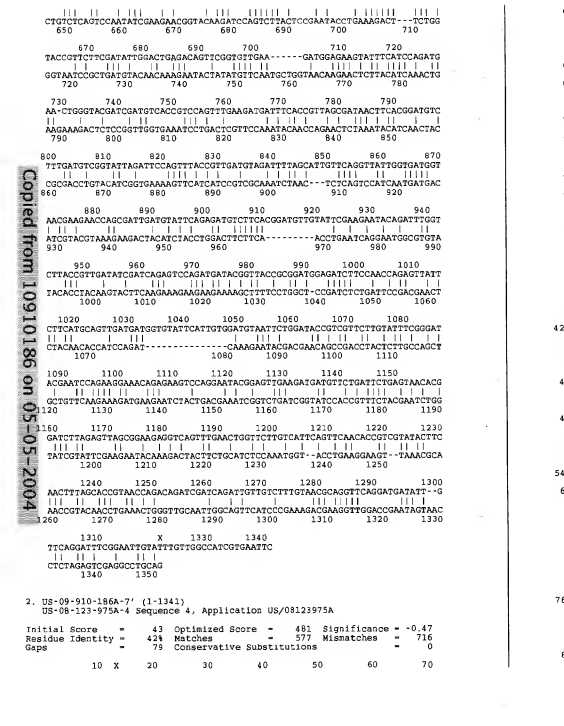
380       390       400       410       420       430       440
    AGGTAGATGTAGTCTTCTTACGTACGATGTCATCATTGATGGACTG---AGAGTTAGATTTGCGACGGATG
    | | |  |  |  |  |  |  |  |||||  |  |  |  |  |   |  |  |  |  |  |  |  |
    CTGATACACATCAATCGCTGGTTCTTCGTTACCATCACCATAACTGAACAATGCTAAAATCTACATCAACG
    440       450       460       470       480       490       500

    450       460       470       480       490       500       510       520
    ATGAACTTTTCACCGATGTACAGGTCGCGGTAGTTGATGTATTTAGAGTTCTGGTTGTATTTGGAACGAGTC
    | |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
    GTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAAC
510       520       530       540       550       560       570       580

          530       540       550       560       570       580       590
    AGGATTTCACCAACCGGAGAGTCTTTCTTCAGTTGATGTAAGAGTTCTTGTTACCAGCATTGAACATATAG
    |  |  | |  |  |  |  |  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |
    TGGACGGTGAC-ATCGATCGTACCCAGTTCATCTGGATGAAATACTTCT------CCATCTTCAACACCGAA
          590       600       610       620       630       640

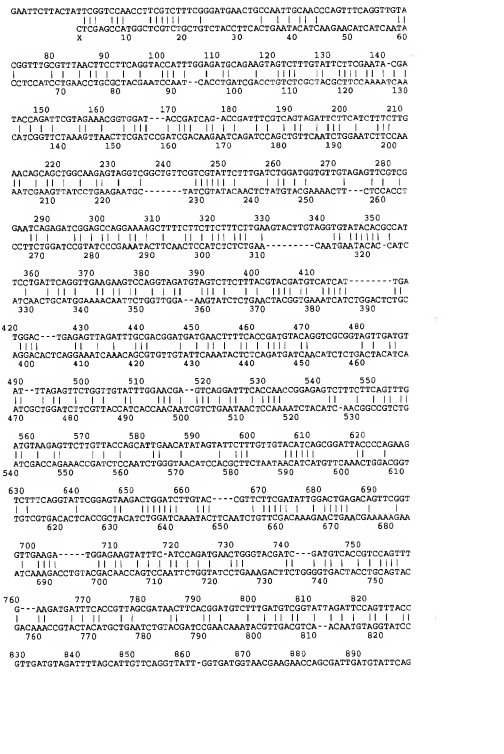
          600       610       620       630       640       650       660
    TATTCTTTGTTGTACATCAGCGGATTACCCCAGA---AGTCTTTCAGGTATTCGGAGTAAGACTGGATCTTG
```

Copied from 10910186 on 05-05-2004



2. US-09-910-186A-7' (1-1341)
US-08-123-975A-4 Sequence 4, Application US/08123975A

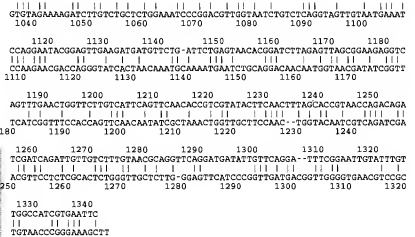
Initial Score = 43 Optimized Score = 481 Significance = -0.47
Residue Identity = 42% Matches = 577 Mismatches = 716
Gaps = 79 Conservative Substitutions = 0



Copied from 10101808 on 05-05-2004

US-09-910-186A-7' (1-1341)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 43 Optimized Score = 481 Significance = -0.47
Residue Identity = 42% Matches = 577 Mismatches = 716
Gaps = 79 Conservative Substitutions = 0



Copied from 10910186 on 05-05-2004

Copied from 10916186 on 05/20/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-8.res made by bobryen on Thu 7 Nov 102 14:32:54-PST.


Query sequence being compared:US-09-910-186A-8 (1-440)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-8 (1-440) with:
          File : USU8123975A.pep
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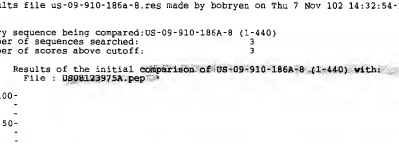



```
                        PARAMETERS

Similarity matrix       PAM-150     K-tuple                    1
Threshold level of sim.    164
Mismatch penalty             1     Joining penalty           20
Gap penalty               5.00     Window size              440
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                     SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                           355          190          144.05

Times:                     CPU                     Total Elapsed
                   00:00:00.00                  00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                                  Init. Opt.
Sequence Name       Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------------
  1. US-08-123-975A-2 Sequence 2, Application U          850   439   439   0.58   0
  2. US-08-123-975A-5 Sequence 5, Application U          439   438   438   0.58   0
                      **** 1 standard deviation below mean ****
  3. US-08-123-975A-3 Sequence 3, Application U          415   189   259  -1.15   0


1. US-09-910-186A-8 (1-440)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   439  Optimized Score  =   439  Significance =  0.58
Residue Identity =    99% Matches          =   438  Mismatches   =     2
Gaps             =     0  Conservative Substitutions             =     0

                    X        10        20        30        40        50
                    MANKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
                    |||||||||||||||||||||||||||||||||||||||||||||||||||
    LKTIMPFDLSIYTNDTILIEMFNKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
            400       410       420       430       440       450       460

            60        70        80        90       100       110       120
    SANSKIRVTQNQNIIFNSVFLDFSVSPWIRIPKYKNDGIQNYIHNETYIINCMKNNSGWKISIRGNRIIWTL
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SANSKIRVTQNQNIIFNSVFLDFSVSPWIRIPKYKNDGIQNYIHNETYIINCMKNNSGWKISIRGNRIIWTL
            470       480       490       500       510       520       530

           130       140       150       160       170       180       190
    IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
            540       550       560       570       580       590       600

           200       210       220       230       240       250       260
    IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
            610       620       630       640       650       660       670

    270       280       290       300       310       320       330       340
    EILTRSKYNQNSKYINYRDLYIGEKFIIRKKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    EILTRSKYNQNSKYINYRDLYIGEKFIIRKKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
    680       690       700       710       720       730       740       750

           350       360       370       380       390       400       410
    KLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    KLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
            760       770       780       790       800       810       820

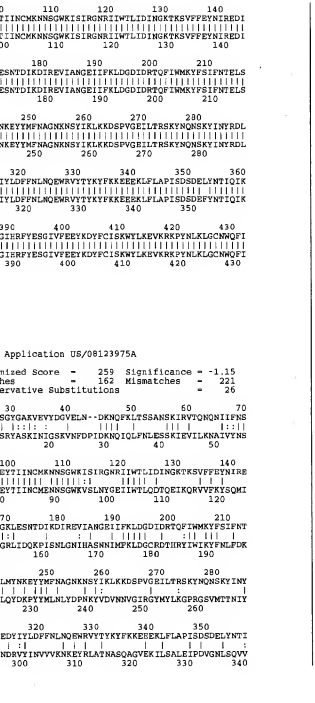
           420       430       X
    LKEVKRKPYNLKLGCNWQFIPKDEGWTE
    ||||||||||||||||||||||||||||
    LKEVKRKPYNLKLGCNWQFIPKDEGWTE
            830       840       850


2. US-09-910-186A-8 (1-440)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   438  Optimized Score  =   438  Significance =  0.58
Residue Identity =    99% Matches          =   437  Mismatches   =     2
Gaps             =     0  Conservative Substitutions             =     0

       X        10        20        30        40        50        60        70
    MANKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    FNKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
    X        10        20        30        40        50        60        70
```

Copied from 10910186 on 05-05-2004



```
        80        90        100       110       120       130       140
LDFSVSFWIRIPKYKNDGIQNYIHNETYIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
LDFSVSFWIRIPKYKNDGIQNYIHNESYIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
        80        90        100       110       120       130       140

    150       160       170       180       190       200       210
SEYINRWFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEYINRWFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
    150       160       170       180       190       200       210

  220       230       240       250       260       270       280
QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGELTRSKYNQNSKYINYRDL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGELTRSKYNQNSKYINYRDL
  220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTIQIK
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDGFYNTIQIK
290       300       310       320       330       340       350

       370       380       390       400       410       420       430
EYDEQPTYSCQLLFKKDRESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
EYDEQPTYSCQLLFKKDRESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
360       370       380       390       400       410       420       430

      440
PKDEGWTE
||||||||
PKDEGWTE
       X


US-09-910-186A-8 (1-440)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =   189  Optimised Score  =   259  Significance = -1.15
Residue Identity =    38% Matches          =   162  Mismatches   =   221
Gaps             =     7  Conservative Substitutions             =    26

          10        20        30        40        50        60        70
MANKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVYQNQNIIFNS
                  ||  | |||| |::|: :  |  |  |  |||| |  |||| |  |:::|
                  RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVTNS
                  X        10        20        30        40        50

          80        90        100       110       120       130       140
VFLDFSVSFWIRIPKYKNDGIQNYIHNETYIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE
  :  |||||||||||| |     |||||||||| |||||:|    ||||| |     | | |
MYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKISQMI
  60        70        80        90        100       110       120

     150       160       170       180       190       200       210
DISEYINRWFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGRIIFKLDGDIDRTQFIWMKYFSIFNT
|||||||||| |||||| |||||||||||||     :  |     | |||||  |   :|| |||  |
NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASWNIMPKLDGCRDTIHRYIWIKYFNLFDK
    130       140       150       160       170       180       190

  220       230       240       250       260       270       280
ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGELTRSKYNQNSKYINY
||  | : |  || |  |||||  | | | |||  |  | |:    |  :  |           |
ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
  200       210       220       230       240       250       260

  290       300       310       320       330       340       350
RDLYIGEKFIIRRKSNSQSINDQIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTI
          |  |  |  |||  | :|       | | |  |  |       |   |  |  |  :
 LNGSLYRGTKFIKKYASGNKDNIVRNNDSVYINVVVKNKEVRLATNASQAGVEKILSALEIPDVGNLSQVV
270       280       290       300       310       320       330       340
```

Copied from 10954186 on 05/25/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9.res made by bobryen on Thu 7 Nov 102 14:42:59-PST.


Query sequence being compared:US-09-910-186A-9 (1-1371)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-9 (1-1371) with:
          File : US08123975A.seq
```

```
                        PARAMETERS

Similarity matrix          Unitary     K-tuple                      4
Mismatch penalty                 1     Joining penalty             30
Gap penalty                   5.00     Window size                500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                     SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            270          241                  52.54

Times:                      CPU                     Total Elapsed
                    00:00:00.00                     00:00:01.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                          Init.  Opt.
Sequence Name     Description                   Length Score Score  Sig.  Frame
-------------------------------------------------------------------------------
                        **** 1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351   331   618  1.16    0
                   **** 0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338   240   620 -0.57    0
  3. US-08-123-975A-1 Sequence 1, Application U   1338   240   620 -0.57    0


1. US-09-910-186A-9 (1-1371)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =   331 Optimized Score  =   618  Significance =  1.16
Residue Identity =   50% Matches         =   706  Mismatches   =   545
Gaps             =   138 Conservative Substitutions =             0

     40         50         60         70         80         90        100
ACACCAACAACTCCCTGTTGAAGGACATCATCAAGGAGTACGTCAACAACATCAACGACTCCAAGATCCTGT
                                  | ||  ||| ||| | | | | | | | | |   ||||||
                                 ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAA---TATCATCCTGA
                                 x         10         20         30        40

    110        120        130        140        150        160        170        180
    CCCTGCAGAACCGTAAGAACACCTTGGTCGACACCTCCGGTTACAACGCCGAGGTCTCCGAGGAGGGTGACG
     |||||  ||   | |||  | ||||   || ||||||  || | ||   | | |  | |  | |  | |  |
     ACCTGCGTTACAAAGCAACAATCTGATCGATCTGTCTGGTTACGGTCTCAAGTTGAAGTATACGACGGTG
50         60         70         80         90        100        110        120

         190        200        210        220        230        240        250
TCCAGCTGAACCCAATCTTCCCATTCGACTTCAAGCTGGGTTCCTCCGGTGAGGACAGAGGTAAGGTCATCG
 | | ||||||     |  |  | ||||| ||  | |||||  |  |  |  |  |||| ||  |  |  |
TTGACTGGATGACAAGAAC------AGTTCAAACTGACCTCTCCCGCT------AACTCTAAGATCCGTG
         130        140        150        160        170        180

      260        270        280        290        300        310        320
TCACCCAGAACGAGAACATCGTCTACAACTCCATGTACGAGTCCTCTCCATCTCCTTCTGGATCAGAATC-
 | || |||| |||||||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
TTACTCAGAATCAGAAGCAATCTTCAACTCCGTAATTCCTCGACTTCCTGTTTCCTTCTGGATCCGTATCC
      190        200        210        220        230        240        250

                330        340        350        360        370
----------AACAAGTGGGTCTCCAACTTGCCA--------GGTTACACCATCATCGACTCCGTCAAGAACA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CGAAATACAAGAACGGTATTCCAGAATTACATCCACAATGAATCCATCATCACTCATCGATGAAGAATA
          260        270        280        290        300        310        320

380        390        400        410        420        430        440        450
ACTCCGGTTGGTCCATCGGTATCATCTCCAACTTCCTGGTCTTCACCCTGAAGCAGAACGAGGACTCCGAGC
 |||| ||||||  ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
ACTCTGGTTGGAAGATCTCCATCCGCGGTAACGGTATCATCTGGACTCTGATCGATATCAAGGTAAGACCA
  330        340        350        360        370        380        390

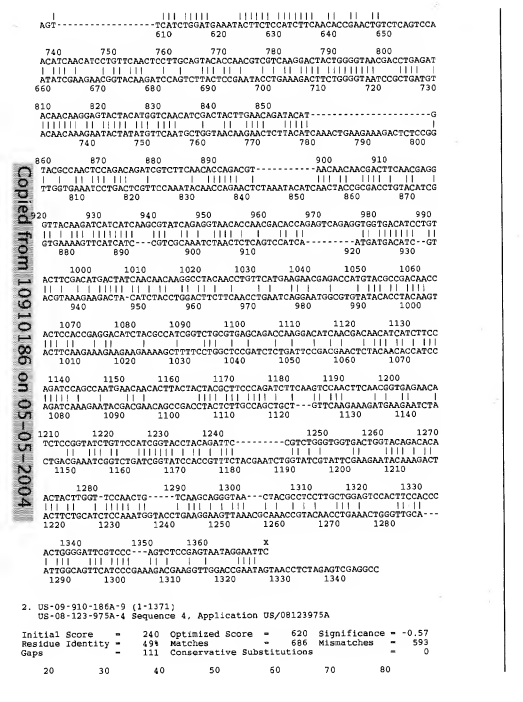
         460        470        480        490        500        510        520
AGTCCATCAACTTCTCCTACGACATCTCCAACAAGGCTCCTGGTTACAACAA----GTGGTCTCTCGTCACCG
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCA
400        410        420        430        440        450        460

         530        540        550        560        570        580        590
TCACCAACAACATGATGGGTAACATGAAGATCTACATCAACGGTAAGCTGATCGACACCATCAAGGTCAAGG
 |||||||| |||  |||  ||  ||||||||||||| | | | | | | | | | | | | | | | | | | |
TCACCAATAACCTGA---ACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAG
470        480        490        500        510        520        530

      600        610        620        630        640        650        660
AGTTGACCGGTATCAACTTCTCCAGACCATCACCTTCGAGATCAACAAGATCCCAGACACGGTCTGATCA
 | | |  | | |  |  |  |  |||| ||  |  |  |  |||| || | | | | | | | | | | | |
ACATCCGTGAAGTTATCGCTAACGGTGAAATCATCT------TCAAACTGGACGGTGACATCGATCGTACCC
540        550        560        570        580        590        600

      670        680        690        700        710        720        730
CCTCCGACTCCGACAACATCAACATGTGGATCCGTGACTTCTACATCTTCGCCAAGGAGTTGGACGGTAAGG
```

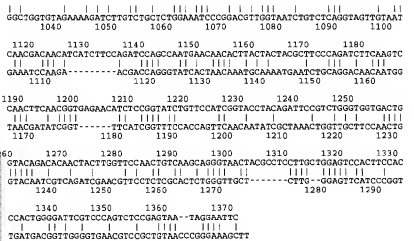
Copied from 10910186 on 05-05-2004



2. US-09-910-186A-9 (1-1371)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	240	Optimized Score	= 620	Significance = -0.57
Residue Identity	=	49%	Matches	= 686	Mismatches = 593
Gaps	=	111	Conservative Substitutions	=	= 0

Copied from 10918618 on 05-05-2004



Copied from 10910186 on 05-05-2004

Copied from 10910186.ob 05/12/2004

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FastPR - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9-inv.res made by bobryen on Thu 7 Nov 102 14:43:14-PST.


Query sequence being compared:US-09-910-186A-9' (1-1371)
Number of sequences searched:          3
Number of scores above cutoff:         3

      Results of the initial comparison of US-09-910-186A-9' (1-1371) with:
        File : US08123975A.seq                          complement

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Copied from 09101186 on 05-05-2004

```
   CATCGATCGTACCCAGTTCATCTGGA---TGAAATACTTCTCCATCTTCAACACCG--AACTGTCTCAGTCC
            600       610       620       630       640       650

790     800       810       820       830       840       850
  GATGGTGTCGATCAGCTTACCGTTGATGTAGATCTTCATGTTACCCATCATGTTGTTGGTGA---CGGTGAC
   |||| | |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||   |||| |||
  AATATCGAAGAAC-GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGAT
  660       670       680       690       700       710       720

 860       870       880       890       900       910       920
   GAAGAACCACTTGTTGTAACCAGAGAGCGTTGTTGG-----AGATGCCATAGGAGAAGTTGATGCACTGCTCG
   | | |||| |  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||
   GTACAACAAAGAATACTA--TATGTTCAATGCTGGTAACAAGAACTCTTACATCCAAACTGAAGAAAGACTCT
  730       740       750       760       770       780       790

      930       940       950       960       970       980       990
  GAGTCCTCGTTCTGTTTCAGGGTAGAACCAGGAAGTTGGAGATACCGATGGACCAACCGGAGTTGTTC
            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   CCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGACTCTAAATACATCAACTACCGGCAGACCTGTAC
  800       810       820       830       840       850       860       870

1000      1010      1020      1030      1040      1050      1060
  TTGACGGAGTCGATGATGGTGTAACCTGGCAGATGGAGACCCACTTGTGATTCTGATCCAGAAGGAGATG
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   ATCGGTGAAAGTTCATCAT---CCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAA
       880       890       900       910       920       930       940

070       1080      1090      1100      1110      1120      1130      1140
  GAGAAGGACTCGTACATGGAGTTGTAGACGATG-TTCTGGTTCTGGGTGACGATGACCTTACTCTGTCCTC
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
   GAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGGGTGTATATACCTACAAGTACTTCAAG
940       950       960       970       980       990      1000      1010

      1150      1160      1170      1180      1190      1200
  ACCGGAGGAACCCAGCTTGAAGTCGAATGG---GAAGATTGGGTTCAGCTGGACGTCACCCTCC---TCGGA
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   AAAGAAGTCGAAAAGCTTGTCCTGGCTCCTGATCCTCGACCAACTCCTACAACACCATCCAGATCAAA
       1020      1030      1040      1050      1060      1070      1080

1210      1220      1230      1240      1250      1260
  GACCTCGGCTTGTAACCGGAGGTGTCGACCAAGGTGTTCTT----------ACGGTCTGC--AGGGACA
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  GAATACGACG-AACAGCACGCACCTACTCTTGCCGAGCTGCTGTTCAAGAAAGATGAGAATCTACTAGCGAAAT
     1090      1100      1110      1120      1130      1140      1150

 1270      1280      1290      1300      1310      1320      1330
  GGATCTTGGAGTCGTTGATGTTGTTGAAGTACTCGTTGATGATGCTCCTCAACAGGGAG-TTGTTGGTGTAG
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  CGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTCCAT
    1160      1170      1180      1190      1200      1210      1220

 1340      1350      1360      1370
  GAGAAGATGTTGAATG--GGATGGTCATCGTGAATTC
   |  |  |  |  |  |  |  |  |  |  |  |  |
  CTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTG
 1230      1240      1250      1260  X   1270      1280
```

2. US-09-910-186A-9' (1-1371)
US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score  =    40  Optimized Score  =   404  Significance  = -0.54
Residue Identity =  40%  Matches         =   495  Mismatches    =   626
Gaps           =    91  Conservative Substitutions              =     0

   190       200       210       220       230       240       250       260
    TGAAGATCGGGAAGCGTAGTAGTAAGTGTTGTTCATTGGCTGGATCTGGAAGATGATGTTGTCGTTGATGT
     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
                CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                X    10        20        30        40        50

         270       280       290       300       310       320       330
```

```
   CCTTGGTCTGCTCACGCAGACCGATGGCGTAG-ATGTCCTCGGTGGAGTG-GTTGTCGGGGTACAATGGTCTC
   | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
     60        70        80        90       100       110       120

          340       350       360       370       380       390       400
   GTTCTTCATGAACAGGTTGTAGGCCTTGTTGTTGATAGTCATGTCGAAGTACAGGATGTCACCACCTCTGAC
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
   AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGT---------TCAA
     130       140       150       160       170       180

      410       420       430       440       450       460       470
   TCTGGTGTCGTTGGTGTTACCTCTGATACGCTTGATGATGATCTTGTAACCCTCGTTGAAGTCGTTGTTGTT
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
   TCTGGAATCTTCCAAAATCGAAGTTATCCTGAGAATGCTATCGTATACACTCTTATGTACGAAACTTCTC
  190       200       210       220       230       240       250

    480       490       500       510       520       530       540
   ACGTCTGGTGTTGAAGACGATCTGTCTGGAGTTGGCGTACATGTATCTGTTCAAGTAGTCGATGTTGACCAT
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   CACCTCCTTCTGGATCCGTATCCGAAATACTCTCAACTCCATCTCTCTGAACAATGAATACCACATCACTAA
260       270       280       290       300       310       320       330

          550       560       570       580       590       600
   GT--------AGTACTCCTTGTTGTATCTCAGGTCGTTACCCCAGT-AGTCCTTGACGACGTTGGTGTAC-T
    |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   CTGCATGGAAACAATCTCGGTTGGAAGTATCTCTGAACTACGGTGAAATCATCCTGCAGGGACAC
             340       350       360       370       380       390       400

610       620       630       640       650       660       670       680
   GCAAGGAGTTGAACAGGATGTTGATGTCCTTACCGTCCAACTCCTTGGCGAAGATGTAGAAGTCACGGATCC
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   TCAGAAATCAAACAGCGTGTTG----------TATTCAAATACTCTCAGATGATCAACATCTCTGACTACA
     410       420       430       440       450       460

          690       700       710       720       730       740       750
   ACATGTTGATGTTGTCGGAGTCGGAGGTGATCAGACCGGTGTCTGGGATCTTGTTGATCTCGAAGGTGATGG
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
   TCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT----------AACTCCAAAATCTACA
     470       480       490       500                   510       520

          760       770       780       790       800       810       820
   TCTTGGAGAAGTTGATACCGGTCAACTCCTTGACCTTGATGGTGTCGATCAGCTTACCGTTGATGTAGATCT
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   TCAACGSCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTC------TAATAACA
     530       540       550       560       570       580             590

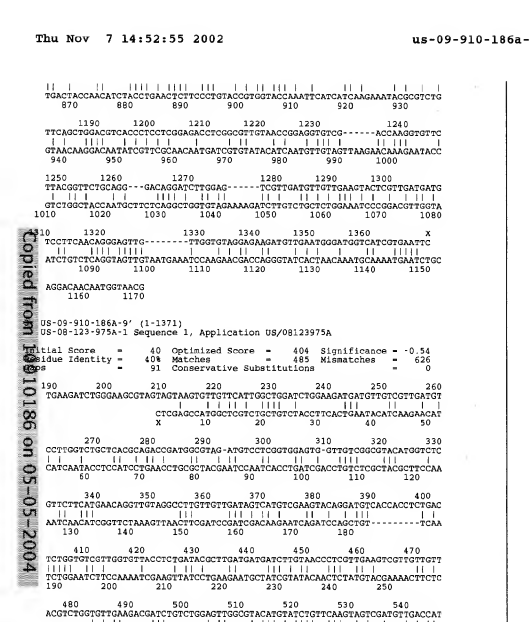
    830       840       850       860       870       880       890
   TCATGTT-ACCCATCATGTTGTTGGTGACGGTGACGAAGAACCACTTGTTGTAACCAGGAGCGTTGTTGGAG
   |||||| |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
   TCATGTTCAAACTGGACGGTTGTCGTGACACTCAC-CGCTACATCTGGATCAAATACTTCAATCTGTTCGA-
       600       610       620       630       640       650       660

    900       910       920       930       940       950       960
   ATGTCGTGAGGAGAAGTTGATGGACTGCTCGGAGTCCTCGTTCGTCTTCAGGGTGAAGACCAGGATTGGAG
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   ----CAAAGAACTGAACGAAAAGAAATCAAAGACCT-GTACGACAACCAGTCCAATTCTGGTATCCTGAAA
           670       680       690       700       710       720

970       980       990      1000      1010      1020      1030
   ATGATACCGATGGACCAACCGGAGTTGTTCTTGACGGAGTCGATGATGGTGTAACCTGGCAGATGGAGACCC
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   GACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTG----AATCT-GTACGATCCGAACA
730       740       750       760       770             780       790

1040      1050      1060      1070      1080      1090      1100      1110
   CACTTGTTGATTCTGATCCAGAAGGAGATGGAGAAGACTCGTACATGGAGTTGTAGACGATGTTCTCGTTC
    |  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
   AATACGTTGA-CGTCAACAATGTAGGTATCCCGCGTTACATGTACCT-GAAAGGTCCGCGTGGTTCT-GTTA
     800       810       820       830       840       850       860

          1120      1130      1140      1150      1160      1170      1180
   TGGGT---GACGATGACCTTACCTCTGTCCTCACCGGAGGAACCCAGCTTGAAGTCGAATGGGAAGATTGGG
```



Copied from 10186 on 05-05-2004

US-09-910-186A-9' (1-1371)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 40 Optimized Score = 404 Significance = -0.54
Identity = 40% Matches = 485 Mismatches = 626
Gaps = 91 Conservative Substitutions = 0

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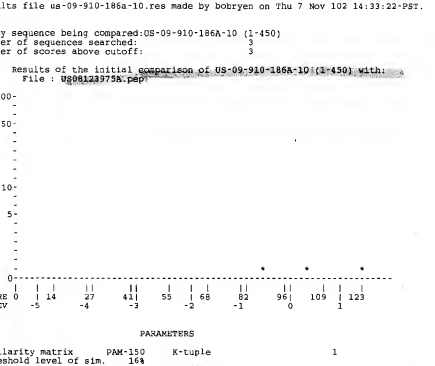
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-10.res made by bobryen on Thu 7 Nov 102 14:33:22-PST.


Query sequence being compared:US-09-910-186A-10 (1-450)
Number of sequences searched:                3
Number of scores above cutoff:               3

      Results of the initial comparison of US-09-910-186A-10 (1-450) with:
        File : US08123975A.pep
```




```
                        PARAMETERS

Similarity matrix          PAM-150      K-tuple                        1
Threshold level of sim.      16%
Mismatch penalty               1      Joining penalty               20
Gap penalty                 5.00      Window size                  450
Gap size penalty            0.05
Cutoff score                   1
Randomization group            0

                      SEARCH STATISTICS

Scores:                      Mean        Median      Standard Deviation
                              104            89                   17.56

Times:                        CPU                     Total Elapsed
                      00:00:00.00                     00:00:01.00

Number of residues:                1704
Number of sequences searched:         3
Number of scores above cutoff:        3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	123	251	1.08	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-5	Sequence 5, Application U	439	103	238	-0.06	0
3. US-08-123-975A-3	Sequence 3, Application U	415	88	229	-0.91	0

```
1. US-09-910-186A-10 (1-450)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   123  Optimized Score  =   251  Significance =  1.08
Residue Identity =    25% Matches         =   121  Mismatches   =   286
Gaps             =    28  Conservative Substitutions =    31

                        X       10        20        30        40        50
                        MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEV
                                  ||        |||   |  :  |  |   |  ||| | :| ||| | |
      KLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTLLEMFNKYNSEILNNILNLRYKDNNLIDLSGYGAKV
          380       390  X    400       410       420       430       440

              60        70        80        90       100       110
      SEEGDVQLNPIFPFDFKLGSSGEDRGKVITVQNENIVYNSMYESFSISFWIRINKWVSN------LPGYTII
                |  |||     |  |  |  |:  |||| |||:||  :  ||:|||||| |  |         |||
      EVYDQVELNDKNQFKLTSSAN----SKIRVTQNQNIIFNSVFLDSVSVSFWIRIPKYKNDGIQNYIHNETTII
         450       460       470       480       490       500       510

      120       130       140       150       160       170       180       190
      DSVKNNSGWSGIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGYNKWFFVTVTNNMMGNMKIYINGKLIDT
        |||||||| | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||||||
      NCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESN
              520       530       540       550       560       570       580

                  200       210       220       230       240       250       260
      IKVKELQGINFSKTITFEINKIPDTGLITSDSDNINMWIRDFYIFAKELDGKDINILFNSLQTTNVVKDYWG
        :::  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||:||
      TDIKDIREVIANGEIIFKLDGDIDRTQF--------IWMKYFSIFNTELSQSNIEERYKIQSTSEYLKDFWG
         590       600       610       620       630       640

              270       280       290       300       310       320       330
      NDLRYNKEYTMVNIDYLNRYMYANSRQIVFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVKGQDILYFDMTIN
        | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      NFLMYNKEYYMPNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGSKFIIRRKSNSQSINDDIV
      650       660       670       680       690       700       710       720

          340       350       360       370       380       390
      NKAYNLFMKNETM--------YADNHSTEDIYAIGLRELQTKDINDNIIFQIQPMNNTIYYASQIFKSNFNGE
        |  :   :   :           |  :   :   :   :   :   :   :   :   :   :   :   :
      RKEDYIYLDFFNLNQEWRVYTIKKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTD
          730       740       750       760       770       780       790

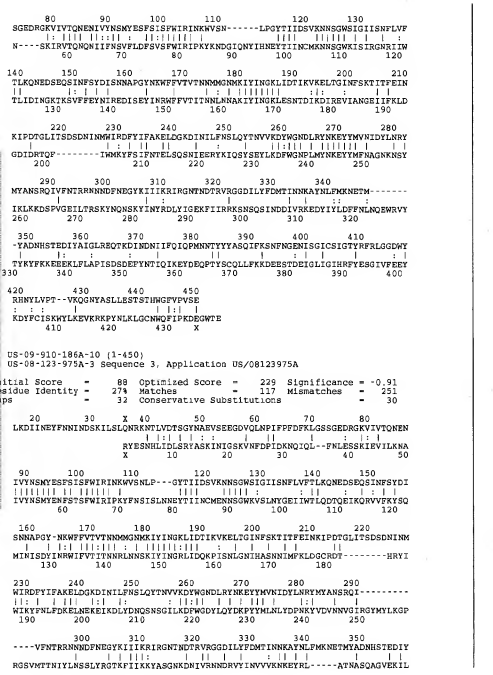
      400       410       420       430       440       450
      NISSICSIGTYFRPLGGDWYRHNYLVPT--VKQGNYASLLESTSFHWGFVPVSE
        |  |  |  |  :  |:  |  :  :           |  |||  |  |  |
      RIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKKPYNLKLGCNWQFIPKDEGWTE
          800       810       820       830       840       X 850

2. US-09-910-186A-10 (1-450)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   103  Optimized Score  =   238  Significance = -0.06
Residue Identity =    25% Matches         =   115  Mismatches   =   274
Gaps             =    28  Conservative Substitutions =    30

             10        20        30        40        50        60        70
      MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPFDFKLGS
                                  ||  |  |  |  |:|  | | | |  |  |  |  |  |  |
                                  FNKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSA
                                  X       10        20        30        40        50
```

Copied from 10/910186 on 05-05-2004



US-09-910-186A-10 (1-450)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 88 Optimized Score = 229 Significance = -0.91
Residue Identity = 27% Matches = 117 Mismatches = 251
Gaps = 32 Conservative Substitutions = 30

Copied from 10914186 05/30/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11.res made by bobryen on Thu 7 Nov 102 14:43:36-PST.


Query sequence being compared:US-09-910-186A-11 (1-1374)
Number of sequences searched:                3
Number of scores above cutoff:               3

          Results of the initial comparison of US-09-910-186A-11 (1-1374) with:
            File : US08123975A.seq

 100-
   -
   -
   -
   -
  50-
   -
   -
   -
   -
   -
   -
   -
   -
  10-
   -
   -
   -
   -
   5-
   -
   -
   -
   -
   -
   -
   -
   -
   0
     |    |    |    |    |    |    |    |    |    |    |    |    |
SCORE 0    50 |  101    151   |202   252|   303    353   |404   454
STDEV      -9   -8    -7    -6    -5    -4    -3    -2    -1    0


                          PARAMETERS

Similarity matrix          Unitary     K-tuple                      4
Mismatch penalty             1         Joining penalty             30
Gap penalty                 5.00       Window size                500
Gap size penalty            0.33
Cutoff score                  1
Randomization group           0

                       SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            431          387          39.26

Times:                      CPU                      Total Elapsed
                      00:00:00.00              00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	454	624	0.59	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	454	624	0.59	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	386	621	-1.15	0

1. US-09-910-186A-11 (1-1374)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score  =   454  Optimized Score  =   624  Significance =  0.59
Residue Identity =  50%  Matches        =   669  Mismatches   =   619
Gaps           =    0%  Conservative Substitutions =    49
```

```
       60        70   X  80        90        100       110       120
CCATTCAACATCTTCTCCTACACCAACAACTCCTTGT-TGAAGGACATCATCAACGAGTACTTCAACTCCAT
                      | | | | |  | | | | |  | | | | |  | | | | |  | | | |  |||
                      CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGACAT
                      X         10        20        30        40        50

  130       140       150       160       170       180       190
CAACGACTCCAAGATCTTGTCCTTGCAGAACAAGAAGAACGCCTTGGTCGACACCTCCGGTTACAACGCCGA
|| | | |  | | | |  | | | |  | | | |  | | | |  | | | |  | | | |  | | | |
CATCAATACCTCCATCCTCGACCTGCGCCTACGAATCCAATCACCTGATGCGACCTGCTCTCGCTACGCTTCCAA
          60        70        80        90        100       110       120

200       210       220       230       240       250       260
GGTCAGAGTCGGTGACAACGTCCAGTTGAACACCATCTACACCAACGACTTCAAGTTGTCCTCTTCCG---G
|||||  ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  |
AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
  130       140       150       160       170       180       190

 270       280       290       300       310       320       330
TGACAAGATCATCGTCAACTTGAACAACAACATCTTGTACTCCGCCAICTACGAGAACTCCTCTGTCTCCTT
| |||| ||| | | | |||| || | | | | | | | | | | | | | | | | | | | | | | | |
TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
 200       210       220       230       240       250       260

340       350       360       370       380       390       400
CTGGATCAAGATCTCCAAGGACTTGA---CCAACTCCC---ACAACGAGTACACCATCATCAACTCCATCGA
|||||||  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTGGATCCGTATCCCGAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCAACTGCATGGA
270       280       290       300       310       320       330       340

  410       420       430       440       450       460       470
GCAGAACTCCGGTTGGAAGTTGTGTATCCGTAACGGTAACATCGAGTGGATCTTGCAGGACGTCAACCGTAA
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAAT
          350       360       370       380       390       400       410

 480       490       500       510       520       530       540
GTACAAGTCCTTGATCTTCGCACTACTCCGAGTCCTTGTCCCACACCGGTTACACCAAACAAGTGGTTCTTCGT
|  ||       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGT
     420       430       440       450       460       470       480

550       560       570       580       590       600       610       620
CACCATCACCAACAACATCATCGGTTACATGAAGTTGTACATCAACGGTGAGTTGAAGCAGTCCCAGAAGAT
 |||||||||||||||  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGAT
  490       500       510       520       530       540       550

          630       640       650       660       670       680       690
CGAGGACCTGGACGAGGTCAAGCTGGACAAGACCATCGTCTTCGGTATCGACGAGAACATCGACGAGAACCA
|   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTCCAATCTGGTAACATCCACGCTTCTAATAACAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCG
 560       570       580       590       600       610       620

      700       710       720       730       740       750       760
GATGTTGTGGATTCGTGACTTCAACATCTTCTCCAAGGAGCTGTCCAACGAGACATCAACATCGTCTACGA
        | | | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

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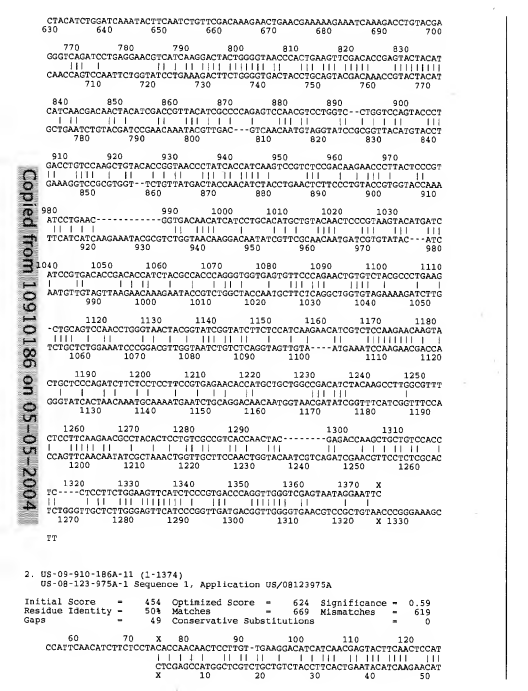

2. US-09-910-186A-11 (1-1374)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	454	Optimized Score	=	624	Significance	=	0.59
Residue Identity	=	50%	Matches	=	669	Mismatches	=	619
Gaps	=	49	Conservative Substitutions				=	0

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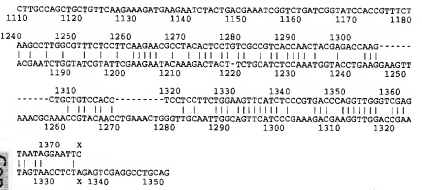
US-09-910-186A-11 (1-1374)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 386 Optimized Score = 621 Significance = -1.15
Residue Identity = 51% Matches = 699 Mismatches = 557
Gaps = 104 Conservative Substitutions = 0



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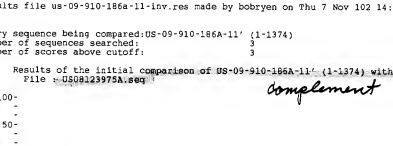
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11-inv.res made by bobryen on Thu 7 Nov 102 14:44:07-PST.

Query sequence being compared:US-09-910-186A-11' (1-1374)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-11' (1-1374) with:
          File = US08123975A.seq
```

complement




```
                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             42           37                   5.77

Times:                      CPU                     Total Elapsed
                   00:00:00.00                  00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	46	308	0.69	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	46	308	0.69	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	36	296	-1.04	0

```
1. US-09-910-186A-11' (1-1374)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score  =     46 Optimized Score  =    308 Significance =  0.69
Residue Identity =  41% Matches          =    366 Mismatches   =   437
Gaps           =     71 Conservative Substitutions =            =     0

         520       530       540       550       560       570       580
GTAACGGTCGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTC
                                    |||| |||||| |||||| |||||| |||||| |||||
                                   CTCGAGCCATGGCCCGTCTGCTGTCTACCTTCACTGAATCATCAAGAACAT
                                  X       10        20        30        40        50

         590       600       610       620       630       640       650
CTTGATGACGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAA
 | | |||| |||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |
CATCAATACCTCATC-----CTGAACCTGCGCTACGAATCCAATCACCTGATCG---ACCTGTCTCGCTAC
         60        70        80        90       100       110

         660       670       680       690       700       710       720
GATGTTGAAGTCACGAATCCACAACATCTGGTCTCGTCGATGTTCTCGTCGATACCGAAGACGATGGTCTT
 |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |
GCT-------TCCAAAATCAACATC----GGTTCT----AAAGTTAACTTCGATCCGATCGACAAGAATCAG
        120       130       140       150       160       170

         730       740       750       760       770       780       790
GTCCAGCTTGACCTCGTCCAGGTCCTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCAT
 |||||| |   |   |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||
ATCCAGCTGTTCAATCTGGA-ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTAT
        180       190       200       210       220       230       240

800       810       820       830       840       850
GTA---------ACCCATGATGTTGTTGGTGATGGTGACGAA------GAACCATTGTTGGTGTAACCGGT
|||         |||  || | | |  | ||||     ||| | |  | |  |  |  |  |  |  |||
GTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCCTGAACAATGA
     250       260       270       280       290       300       310

     860       870       880       890       900       910       920
GTGGGACAAGGACTCGGAGTAGTCGAAGATCAAGGACTTGTACTTACGGTTGACGTCCTGCAAGAATCCACTC
 | ||  |  |  |  | | |  | | | | | |  | | | | | |  | | | | | |  | | | | | |
ATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTG
     320       330       340       350       360       370       380

930       940       950       960       970       980       990
GATGTTACCGTTACGGATACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTT
||  | | |  | |  | | | |||  | |  | |  | |  | |  | |  | |  | |  | |  | |
GACTCTGCAG---GACACTCAGGAAATCAAACAGCCGTTTGTATTCAAATACTCTCAGATGATCAAC---AT
390       400       410       420       430       440       450

1000      1010      1020      1030      1040      1050      1060      1070
GTGGGAGTTGGTCAAGTCCTTGGAGATCTTGATCCAGAAGGAGACAGAGGAGTTCTCGTAGATGGCGGAGTA
 | | |  |||  | |  | |  | |  | |  | |  | |  | |  | |  | |  | |  | |  | |
CTCTGACTACATCAATCAGTCCTGGATCTTCGTTACCATCACAACAATCGTCTGAATAACTCCAAAATCTACAT
     460       470       480       490       500       510       520

         1080      1090      1100      1110      1120      1130      1140
CAAGATGTTGTTGTTCAAGTTGACGATGATCTTGTCACCGGAAGAGGACAACTTGAAGTCGTTGGTGTAGAT
|||  | |  | |  |  |||| |  | |  | |  | |  | |  | |  | |  | |  | |  | |  | |
CAACGGCCGTCTGATCGACCAGAAACCGATCT------CCAATCTGGGTAACATCCACGCTTCTAATAACAT
 530       540       550       560       570       580       590

    1150      1160      1170      1180      1190      1200      1210
GGTGTTC-AACTGGACGTTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTCGACCAAGGCGTTCT
 |||||| |||||||| |  |||| | | | | | | | | | | | | | | | | | | | | | | |
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CATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCG---A
      600       610       620       630       640       650       660

1220      1230      1240      1250      1260      1270      1280
TCTTGTTCTGCAAGGACAAGATCTTGGAGTCGTTGATG-----GAGTTGAAGTACTCGTCGATGATGTCCTT
   |  |||  | |  ||||  |  || | |  |||  | |  |||  |||  | |  ||  |||  |||
CAAAGAACTGAACGAGAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTT
      670       680       690       700       710       720       730

1290      1300      1310      1320      1330      1340
CAACAAGGAGTTGTTGGTGTAGGAGA---------AGATGTTGAATGGCATGGTGTTCTCGAAGGACTCGTT
|  ||| |  ||  ||| ||  |  |  |  |  | |||||  |  |  ||  |  |  |  |  ||||
CTGGGCTGACTACCGACTACGACAAACCGTACTACATGCTGAAT--CTGTACGATCGGAACAAAGACGTT
      740       750       760       770       780       790       800

1350      1360      1370  X
GACCTTAGCCTTCAAACGCATCGTGAATTC
|| |  |  |  |  |  |  |  |  |||
GACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
    810       820       830  X   840       850

US-09-910-186A-11' (1-1374)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    46  Optimized Score  =    308  Significance =  0.69
Residue Identity =   41%  Matches          =    366  Mismatches   =  437
Gaps             =    71  Conservative Substitutions =              =    0

      520       530       540       550       560       570       580
GTAACGGTCGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTC
                  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
                CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                X        10        20        30        40        50

      590       600       610       620       630       640       650
CTTGATGACGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAA
| | | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CATCAATACGTCCATC----CTGAACCTGCGCTACGAATCCAATCACCTGATCG----ACCTGTCGTCGCTAC
      60        70        80        90       100       110

      660       670       680       690       700       710       720
GATGTTGAAGTCACGAATCCACAACATCTGGTTCTCGTCGATGTTCTCGTCGATACGGAAGACGATGGTCTT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GCT-------TCCAAAATCAACATC----GGTTCTC----AAAGTTAACTTCGATCCGATCGACAAGAATCAG
      120       130       140       150       160       170

  730       740       750       760       770       780       790
GTCCAGCTTGACCTCGTCCAGGTCCTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCAT
|  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ATCCAGCTGTTCAATCTGGA-ATCTTCAAAATCGAAGTTATCCTGAAGAATGCTATCGATATCAAGTTCAA
      180       190       200       210       220       230       240

800                   810       820       830       840       850
GTA---------ACCCATGATGTTGTTGGTGATGGTGACGAA------GAACCACTTGTTGGTGTAACCGGT
|||         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCGGAAATACTTCAACTCCATCTCTCGACAATGA
     250       260       270       280       290       300       310

  860       870       880       890       900       910       920
GTGGGACAAGGACTCGGAGTAGTCGAAGATCAAGGACTTGTACTTACGGTTGACGTCCTGCAAGATCCACTC
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTG
  320       330       340       350       360       370       380

  930       940       950       960       970       980       990
GATGTTACCGTTACGGATACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTT
|  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
 GACTCTGCAG---GACACTCAGGAAATCAAACAGCGTGTTGTTATTCAAATACTCTCAGATGATCAAC---AT
390       400       410       420       430       440       450

1000      1010      1020      1030      1040      1050      1060      1070
GTGGGAGTTGGTCAAGTCCTTGAGAATCTTGATCCAGAAGGAGACAGAGGAGTTCTCGTAGATGGCGGAGTA
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                                                                  |  |  |
CTCTAACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACAT
      460       470       480       490       500       510       520

      1080      1090      1100      1110      1120      1130      1140
CAAGATGTTGTTGTTCAAGTTGACGATGATCTTGTCACCGGAAGAGGACAACTTGAAGTCGTTGGTGTAGAT
|||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CAACGGCCGTCTGATCGACCAGAAACCGATCT-------CCAATCTGGGTAACATCCACGGTTCTAATACAT
  530       540       550       560       570       580       590

     1150      1160      1170      1180      1190      1200      1210
GGTGTTC-AACTGACGTTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTCGACCAAGGCGTTCT
|||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCG---A
      600       610       620       630       640       650       660

  1220      1230      1240      1250      1260      1270      1280
TCTTGTTCTGCAAGGACAAGATCTTGGAGTCGTTGATG-----GAGTTGAAGTACTCGTCGATGATGTCCTT
   |  |||  | |  ||||  |  || | |  |||  | |  |||  |||  | |  ||  |||  |||
CAAAGAACTGAACGAGAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTT
      670       680       690       700       710       720       730

  1290      1300      1310      1320      1330      1340
CAACAAGGAGTTGTTGGTGTAGGAGA---------AGATGTTGAATGGCATGGTGTTCTCGAAGGACTCGTT
|  ||| |  ||  ||| ||  |  |  |  |  | |||||  |  |  ||  |  |  |  |  ||||
CTGGGCTGACTACCGACTACGACAAACCGTACTACATGCTGAAT--CTGTACGATCGGAACAAAGACGTT
      740       750       760       770       780       790       800

  1350      1360      1370  X
GACCTTAGCCTTCAAACGCATCGTGAATTC
|| |  |  |  |  |  |  |  |  |||
GACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
    810       820       830  X   840       850

3. US-09-910-186A-11' (1-1374)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    36  Optimized Score  =    296  Significance =  -1.04
Residue Identity =   40%  Matches          =    349  Mismatches   =   468
Gaps             =    44  Conservative Substitutions =              =     0

      520       530       540       550       560       570       580       590
CGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTCCTTGATGA
                  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
                ATGGCTTTCAACAAATACAATTCCGTCGAAATCCTGAACAATATCATCCTGA--A
                X        10        20        30        40        50

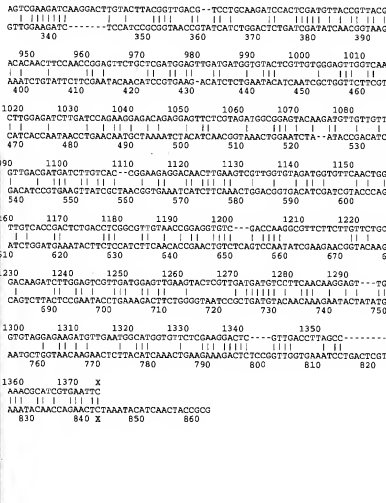
      600       610       620       630       640       650       660
CGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAAGATGTTGA
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGT
      60        70        80        90       100       110       120

  670       680       690       700       710       720       730
AGTCACGAATCCACAACATCTGGTTCTCGTCGATGTTCTCGTCGATACGGAAGACGATGGTCTTGTCCAGCT
|  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TGAACTGAAI-GACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGA--TCCGTGTTACTCAGAA
      130       140       150       160       170       180       190

  740       750       760       770       780       790       800
TGACTCGTCCAGGTCC-CTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCATGTA-AC
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCCTCGTTTCCTTCTGGATCCGTATCCCGAAATACAA
      200       210       220       230       240       250       260

      810       820       830       840       850       860       870
CCATGATGTTGTTGGTGATGGTGACGAAGAACCACTTGTTGGTGTAACCGGTGTGGGACAAGGACTCGGAGT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCAT-GAAGAATAACTCTG---
      270       280       290       300       310       320       330

  880       890       900       910       920       930       940
```



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Copied from 10916186 on 05/20/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-12.res made by bobryen on Thu 7 Nov 102 14:33:46-PST.


Query sequence being compared:US-09-910-186A-12 (1-451)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-12 (1-451) with:
          File : US08123975A.pep
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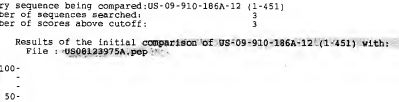


```
                                PARAMETERS

Similarity matrix          PAM-150     K-tuple                        1
Threshold level of sim.        16%
Mismatch penalty                 1     Joining penalty               20
Gap penalty                   5.00     Window size                  451
Gap size penalty              0.05
Cutoff score                     1
Randomization group              0

                            SEARCH STATISTICS

Scores:                      Mean        Median      Standard Deviation
                              147           120           29.05

Times:                        CPU                       Total Elapsed
                      00:00:00.00                    00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best_scores is:

                                                                  Init. Opt.
Sequence Name      Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------------
                    **** 1 standard deviation above mean ****
  1. US-08-123-975A-3 Sequence 3, Application U      415   177   236  1.03   0
                    **** 0 standard deviation from mean ****
  2. US-08-123-975A-2 Sequence 2, Application U      850   145   265 -0.07   0
  3. US-08-123-975A-5 Sequence 5, Application U      439   119   244 -0.96   0


1. US-09-910-186A-12 (1-451)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    177  Optimized Score  =    236  Significance =  1.03
Residue Identity =    26%  Matches         =    109  Mismatches   =   267
Gaps             =      8  Conservative Substitutions =             =    28

     30        40        50        60        70        80        90
  LKDIINEYFNSLNDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDFKL-SSSGDKIIVNLNNNIL
                                                                  RYESNHLIDLSRVASKINQSSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                                                                  X        10        20        30        40        50

   100       110       120       130       140       150       160
  YSAIYENSSVSFWIKISK--DLTNSHNEYTIINSIEQNSNGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESL
  YNSMFSNFDSFWIKIFKYFNSISLKNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQETKQRVVFKYSQMI
        60        70        80        90       100       110       120

   170       180       190       200       210       220       230       240
  SHTGYTNKWFFVTITNNLMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSK
  NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
     130       140       150       160       170       180       190

           250       260       270       280       290       300       310
  ELSNED:NIVYEGQLRNVIKDYWGNPLKFDTEYYIINDNYIDRVIAPESNVLVLVQYPDLSKLYTGNPITI
  ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
   200       210       220       230       240       250       260

           320       330       340       350       360       370
  KSVSDNKPYSRILN------GDNIILHMLYNSKKYMIIRDTDTIYATQGGRCSQNCVYALKLQSNLGNYGIGI
  LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
 270       280       290       300       310       320       330       340

 380       390       400       410       420       430       440       450
  FSIKNIVSKNKYCSQIFSSFRENTMLLADLYKPWRFSFKNATPVAVINTETKLLSTSFWKFISRDFGPWVE
  VMKSKNDQGITNKCKMMLQONNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLQCSWEFIPVDDGWGS
        350       360       370       380       390       400       410 X

  RPL


2. US-09-910-186A-12 (1-451)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    145  Optimized Score  =    265  Significance = -0.07
Residue Identity =    30%  Matches         =    147  Mismatches   =   273
Gaps             =     31  Conservative Substitutions =             =    25

                  X        10        20        30        40        50
                  MRLKAKVNESFENTMPFNIFSVTNNSLLKDDINEYFNSINDSKILSLQNKKN
  LKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNILNLRYKDN
        370       380       390       400       410       420       430

        60        70        80        90       100       110       120
  ALVDTSGYNAEVRVGDNVQLNTIYTNDFKLSSSGDKIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---
```

Copied from 10910186a on 05-05-2004

US-09-910-186A-12 (1-451)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 119 Optimized Score = 244 Significance = -0.96
Identities = 30% Matches = 136 Mismatches = 255
Gaps = 31 Conservative Substitutions = 23

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13.res made by bobryen on Thu 7 Nov 102 14:44:27-PST.

Query sequence being compared:US-09-910-186A-13 (1-1400)
Number of sequences searched:          3
Number of scores above cutoff:         3

          Results of the initial comparison of US-09-910-186A-13 (1-1400) with:
            File : US08123975A.seq
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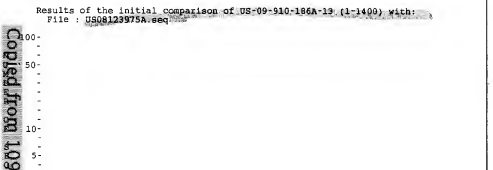


```
                              PARAMETERS

Similarity matrix          Unitary      K-tuple                        4
Mismatch penalty                 1      Joining penalty               30
Gap penalty                   5.00      Window size                  500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                           SEARCH STATISTICS

Scores:                      Mean        Median      Standard Deviation
                              392           323           60.62

Times:                        CPU                   Total Elapsed
                      00:00:00.00                   00:00:00.00

Number of residues:             4027
Number of sequences searched:      3
Number of scores above cutoff:     3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	427	692	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	427	692	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	322	612	-1.15	0

```
1. US-09-910-186A-13 (1-1400)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score  =   427  Optimized Score  =   692  Significance =  0.58
Residue Identity =  54%  Matches        =   739  Mismatches   =   539
Gaps           =    72  Conservative Substitutions =             0

      70        80        90       100       110       120       130       140
TCCTTTTAAGCTTCTTCTTATACAGATGATAAAATTTTAATTTCCTACTTCCAACAAGTTCTTCAAGAGAAT
                                    ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
                          CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                          X         10        20        30        40        50

     150       160       170       180       190       200       210
TAAGTCTTCTTCCGTTTTAAACATGAGATACAAGAATGATAAATACGTCGACACTTCCGGTTACGACTCCAA
   |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
        60        70        80        90       100       110       120

      220       230       240       250       260       270       280
TATCAACATTAACGGTGACCTGTACAAGTACCCAACTAACAAAAACCAATTCGGTATCTACAACGACAAGCT
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
        130       140       150       160       170       180       190

      290       300       310       320       330       340       350
TTCCGAGGTCAACATCTCTCAAAACGACTACATTATTACGACAACAAGTACAGAACTTCTCTATTTCTTT
|||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
 200       210       220       230       240       250       260

      360       370       380       390       400       410       420
CTCGGTCAGGATTCCTAACTACGCAACAAGATCGTCAACGTTAACAACGAGTACACTATCATCAACTGTAT
|||| || | || || || ||||  | | ||  | ||||| | |||||||||| || ||||||||||| ||
CTGGATCCGTATCCGAAATACTTCAAC---TCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT
270       280       290       300       310       320       330

430       440       450       460       470       480       490       500
GAGAGACAACAACTCCGGTTGGAAGGTTCTCTTAACCACACGAGATATCTTTGGACCTTGCAAGACAACGC
|  || |||| || |||||||| || |||| ||| ||  | |||| |||| |||| ||||
G---GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
   340       350       360       370       380       390       400

      510       520       530       540       550       560       570
AGGTATTAACCAAAAGTTAGCATTCAACTACGGTAACGCAAACGGTATTTCTGACTACATCAACAAGTGGAT
 | || || |  | |||||| ||| | |  | | ||  |||||||||||||||||||||||||||||||||||
CGAAATCAACAGCGGTTGTTATTCAAATACTCTCAGATGATCAACATCTCGTACTACATCAATCGCTGGAT
 410       420       430       440       450       460       470

      580       590       600       610       620       630       640
TTTCGTCACTATCACTAACGACAGATTAGGTGACTCTAAGCTTTACATTAACGGTAACTTAATCGACCAAAA
 |||||| || |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTTCGTTACCATCACCAACACAGATCGTCTGAATAACTCCAAACTCACATCAACGGCGTCTGATCGACCAGAA
480       490       500       510       520       530       540       550

      650       660       670       680       690       700       710
GTCCATTTTAAACTTAGGTAACATTCACGTTTCTGACAACATCTTATTCAAGATCGTTAACTGCAGTTACAC
 | | | | | | | |||||| |||| |||| | | |||||  | | | | | | | | | | ||  |||
ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAAACATCATGTTCAACTGCAGCGGTCGTCGTGACAC
        560       570       580       590       600       610       620

      720       730       740       750       760       770       780
---CAGATACATTGGCATTAGATACTTCAACATTTTCGACAAGGAGTTAGACGAGACCGAGATTCAAACTTT
   | | |||||  | | | |||||||||| | |||||||| || | | | | | | | | | | | | |
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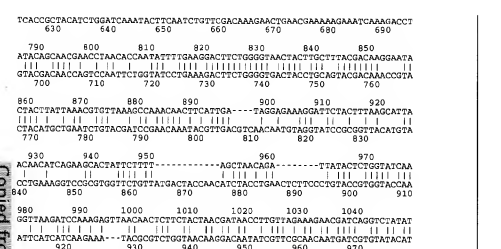
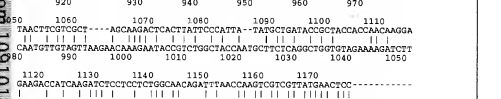
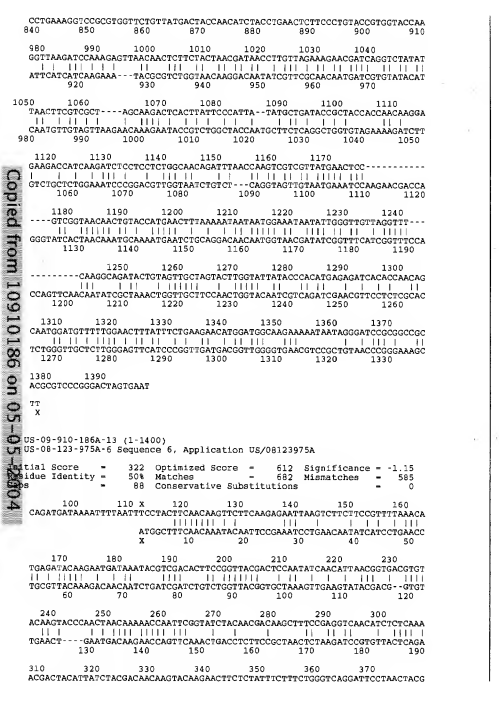


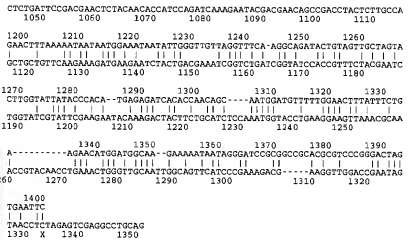
2. US-09-910-186A-13 (1-1400)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	427	Optimized Score	=	592	Significance	= 0.58
Residue Identity	=	54%	Matches	=	739	Mismatches	= 539
Gaps	=	72	Conservative Substitutions	=			= 0



Copied from 10910186 on 05-05-2004





Copied from 10910186 on 05-05-2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13-inv.res made by bobryen on Thu 7 Nov 102 14:44:44-PST.


Query sequence being compared:US-09-910-186A-13' (1-1400)
Number of sequences searched:              3
Number of scores above cutoff:             3

      Results of the initial comparison of US-09-910-186A-13' (1-1400) with:
        File : US08123975A.seq
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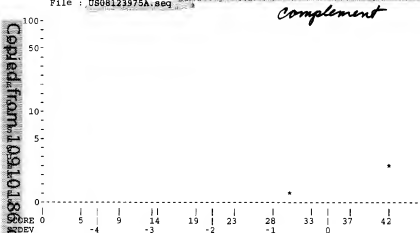
Complement




```
                        PARAMETERS -

Similarity matrix          Unitary    K-tuple                        4
Mismatch penalty             1        Joining penalty               30
Gap penalty                  5.00     Window size                  500
Gap size penalty             0.33
Cutoff score                 1
Randomization group          0

                        SEARCH STATISTICS

Scores:                    Mean       Median    Standard Deviation
                             38           31          6.93

Times:                      CPU                   Total Elapsed
                      00:00:00.00           00:00:00.00

Number of residues:          4027
Number of sequences searched:   3
Number of scores above cutoff:  3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	42	273	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	42	273	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	30	480	-1.15	0

```
1. US-09-910-186A-13' (1-1400)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    42  Optimized Score  =   273  Significance =  0.58
Residue Identity  =    42% Matches          =   333  Mismatches   =   384
Gaps              =    68  Conservative Substitutions            =     0

                    X       10        20        30        40
                    GAATTCACTAGTCCCGGGACGCGTGCGGCCGC----GGATCCCTATTATTTT
                    |||||| | | | | | | | | | | | | | | | | | | | | | | | |
      TTCTAAATAACATCATGTTCAAACTGGACGGTTCGTCGTGACCACTCACCCTCACATCTGGTACAAATACTTCAA
            590       600       610       620       630       640       650

      50        60        70        80                90       100       110
      TCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAA---------AACATCCATTGCTGTTGGTGTGATCT
      |||| | | | | | | | | | | | | | | | | | | |
```

Created from 10910186 on 05-05-2004

```
GGTTTCCACCAGTTCAA---CAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGT
   1190      1200          1210      1220      1230      1240      1250

680       690       700       710       720       730       740       750
ATCTGGTGTAACTGCAGTTAACGACTTGAATAAGATGTTGTCAGAAACGTGAATGTTACCTAAGTTTAAAA
  ||| |||| |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
   1260      1270      1280      1290      1300      1310      1320

          760  X  770       780
TGGACTTTTGGTCGATTAAGTTACCGTTAATGT
  ||| |||| |||  |||||||||||||||||
CCCGGGAAAGCTT
  1330      X

2. US-09-910-186A-13' (1-1400)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    42  Optimized Score  =   273  Significance =  0.58
Residue Identity  =   42%  Matches          =   333  Mismatches   =  384
Gaps              =    68  Conservative Substitutions             =    0

                      X      10        20        30        40
                      GAATTCACTAGTCCCGGGACGCGTGCGGCCGC----GGATCCCTATTATTTT
                      |||  |||  |||||  |||  |||||  ||||    |||||  |||||||
TTCTAAATAACATCATGTTCAAACTGGACGGTTGCTGGACACTCACCGCTACATCTGGATCAAATACTTCAA
      590       600       610       620       630       640       650

50        60        70        80        90       100       110
TCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAA---------AACATCCATTGCTGTTGGTGTGATCT
|||  | | | ||  | ||||  |||||||||||||||         ||| |||| |  ||  ||||  ||
TCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCT
      660       670       680       690       700       710       720

          120       130       140       150       160       170
----CTCATGTGGTATAATACC--AAGTACTAGCAACTACAGTATCTGCCTTGAAACCTAACAACCCAATA
    |  | ||||  | ||||  ||||| |  |||  | ||  |||| ||||  |  | |  |
GAAAGACTTCTGGGTACTACCTGCAGTACGACAAACCGTACTACATGC--TGAATCTGTACGATCCGAAC
  730       740       750       760       770       780       790

180       190       200       210       220       230       240
TTATTTCCATTATTATTTTTAAAGTTCATGGTACAGTTGTTACCGACGGAGTTCATAACGACGACTTGGTTA
AAAT----ACGTTGACGTCACAACATGTAGGTATCCGCGGTTAC--ATGTACTGA-AAGTCCGCGTGGT---
     800       810       820       830       840       850

250       260       270       280       290       300       310       320
AATCTGTTGCCAGAGGAGGAGTCTTGATGGTCTTCTCCTTGT-TGGTGGTAGCGGTATCAGCATATAATGG
 ||||||  | |  |  |  |||  |  |||  |||||||| |||||||||||||||||||||||||||||
---TCTGTTATGA-CTACCAACAGTCACTGAACCTTCCCTGTACCTGGTGACAAATCATCATCACTAA---G
   860       870       880       890       900       910       920

330       340       350       360       370       380       390
GAATAAGTGAGTCTTGCTAGCGACGAAGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTATCGTTAGT
|||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAATACGCGTCT----------GGTAACAAGGACAATATCGTTCGCAACAATGATCGGTGTATACATC
     930                       940       950       960       970       980

400       410       420       430       440       450       460
AGAAGAGTTGTTAACTCTTTGGATCTTAACCTTGATACCAGAGTATAATCTGTTAGCTAAAAGAATAGTGCT
|| ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATGTTGATGTTAGAACAAAGAATACGGTCTGCTACCATACTCTTCTCAGGCTGGTGTAGAAAAGATCTTG
      990      1000      1010      1020      1030      1040      1050

470       480       490       500       510       520       530
TCTGATGTTGTTAATGCTTAAAGTAGAATCCTTTCTCCTATCAATGAAGTTGTTTGGCTTTAACACGTTTAA
|||| | |  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTC----------AGGTAGTTGTAATGAAATCCAAGAA
     1060      1070      1080                1090      1100      1110

540       550       560       570       580       590       600
TAAGTAGTATTCCTTGTCGTAAAGCAAGTAGTTACCCAGAAGTCCTTCAAAATATTGGTGTTAGGTTCGTT
```

```
                                                  |  ||  |  |  || ||||  | |  |  |  |  |  |  |  |||  |
CGACCAGGGTATCACTAACAAATGCAA--AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATC
   1120      1130      1140      1150      1160      1170      1180

610       620       630       640       650       660       670
GCTGTATAAAGTTTGAATCTCGGTCTCGTCTAACTCCTTG-TCGAAAATGTTGAAGTATCTAATGCCAATGT
| | | |  |  ||  |  | |||  | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GGTTTCCACCAGTTCAA---CAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGT
   1190      1200      1210      1220      1230      1240      1250

680       690       700       710       720       730       740       750
ATCTGGTGTAACTGCAGTTAACGACTTGAATAAGATGTTGTCAGAAACGTGAATGTTACCTAAGTTTAAAA
||  |||| |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
   1260      1270      1280      1290      1300      1310      1320

          760  X  770       780
TGGACTTTTGGTCGATTAAGTTACCGTTAATGT
  ||| |||| |||  |||||||||||||||||
CCCGGGAAAGCTT
  1330      X

3. US-09-910-186A-13' (1-1400)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    30  Optimized Score  =   480  Significance = -1.15
Residue Identity  =   41%  Matches          =   572  Mismatches   =  715
Gaps              =    10  Conservative Substitutions             =    0

40        50        60        70        80        90       100       110
CTATTATTTTTCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAAAACATCCATTGCTGTTGGTGTGATC
                  ATGGCTTTCACAACAAATACAATTTCCGAAAATCCTGAA-------CAATATCATC
                  X        10        20        30                40

          120       130       140       150       160       170       180
TCTCATGTGGGTATAATACCAAGTACTAGCAACTACAGTATCTGCCTTGAAAC-CTAACAACCCAATATTAT
    |  | ||||  | ||||  ||||| |  |||  | ||  |||| ||||  |  | |  |
CTGAACCTGCGT----TACAAAG-ACAACAATCTGATCCATCTGTCTGGTTACGGTGCTAAAGTTGAAGTAT
  50        60        70        80        90       100       110

190       200       210       220       230       240       250
TTCCATTATTATTTTTAAAGTTCATGGTACAGTTGTTACCGACGGAGTTCATAACGACGACTTGGTTAAATC
ACGACGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCC---GCTAACTCTAAGATCCGTG
     120       130       140       150       160       170       180

260       270       280       290       300       310       320
TGTTGCCAGAGGAGGAGATCTTGATGGTCTTCTCCTTGTTGGTGGTAGCGGTATC--------------AGCA
|  |  |  |  |||  |  |||  |||||||| |||||||||||||||||||||||||||||||||||||
TTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTCCTTCTGGATCCGTATCC
     190       200       210       220       230       240       250

320       330       340       350       360       370       380
TATAATGGGAATAAGTGAGTCTTGCTAGCGACGAAGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTA
|||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATA
     260       270       280       290       300       310       320

390       400       410       420       430       440       450
TCGTTAGTAGAAGAGTTGTTAACTCTTTGGATCTTAACCTTGATAC----CAGAGTATAATCTGTTAGCTAA
|||  |||| ||||||||||||||||||||||||||||||||||||    |||||||||||||||||||||||
ACTCTGGTTGGAAGATCTCCATCCGCGGTAACGGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCA
  330       340       350       360       370       380       390

460       470       480       490       500       510       520
AAGAATAGTGCTTCTGATGTTGTTAATGCTTAAAGTAGAATCCTTTCTCCTATCAATGAAGTTGTTTGGCTT
||  |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTG--GTTCTTCGTTAC
400       410       420       430       440       450       460

    530       540       550       560       570       580       590
```

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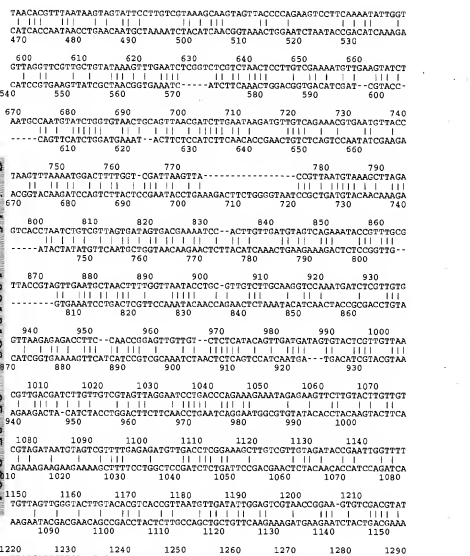

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-14.res made by bobryen on Thu 7 Nov 102 14:34:07-PST.

Query sequence being compared:US-09-910-186A-14 (1-449)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-14 (1-449) with:
          File : US08123975A.pep
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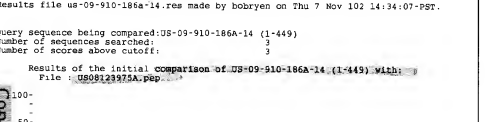


```
                        PARAMETERS

Similarity matrix          PAM-150    K-tuple                    1
Threshold level of sim.        16%
Mismatch penalty                1    Joining penalty           20
Gap penalty                  5.00    Window size              449
Gap size penalty             0.05
Cutoff score                    1
Randomization group             0

                     SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            153          144                   8.66

Times:                      CPU                     Total Elapsed
                   00:00:00.00                  00:00:00.00

Number of residues:                    1704
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
1. US-08-123-975A-5	Sequence 5, Application U	439	158	247	0.58	0
2. US-08-123-975A-2	Sequence 2, Application U	850	158	271	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-3	Sequence 3, Application U	415	143	276	-1.15	0

```
1. US-09-910-186A-14 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score   =   158  Optimized Score  =   247  Significance =  0.58
Residue Identity =   31%  Matches         =   141  Mismatches   =   233
Gaps             =    35  Conservative Substitutions            =    34

      20        30        X 40        50        60        70        80
NNSIPFKLSSYTDDKILISYFNKFPKRIKSSSVLMMRYKNDKYVDTSGYDSNIYINGDVYKPTNKNQFGIY
                          |||:  |   |:|:|||    :| ||| : : :  |    ||||
                          FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGV--ELNDKNQFKLT
                          X        10        20        30        40        50

      90       100       110       120       130       140       150
NDKLSEVNISQNDYIIYDNKYKWFSISFWVRIPNYDNKIVN--VNNEYTIINCMNDNNSGWKVSLNHNEIIW
  | : : ||  ||:   :  |||:|||:||| | |  :   : ||||||||: ||||||:|    | |||
SSANSKIRVTQNQNIIPNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIW
         60        70        80        90       100       110       120

160       170       180       190       200       210       220       230
TLQDNAGINQKLAFNYGNANGISDYINKWIFVTITNDRLQDSKLYINGNLIDQKSILNLGNIHVSDNILFKI
|| |  |     | |    ||:|||:| ||||||  |  :| |||| |     |   |  :    | ||
TLIDINQKTKSVFFEVNEDISEYINWFWFVTITNN-LANNAKIYINGKLESNTDIKDIREVIANGEIIFKL
      130       140       150       160       170       180       190

      240       250       260       270       280       290       300
-VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRKKDS
 :|  :|| |  |  |  ||  |  |  |  |  |  |||||| |:| |||| :  | |  : |  :|||
DGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYELKLKDS
      200       210       220       230       240       250       260

      310       320       330       340       350       360
TLSINNIRSTLLLANRLYSGIKVKI-------QRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATT
 ||    :  |  |  |  |  |  |       :| |  || |||  | :|  |
PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRSRSNSQSINDDIVRKEDYILQFFNLNQEWRVYTYKYFKK
  270       280       290       300       310       320       330

 370       380       390       400       410       420
NKEKTIKISSSG-----NRFNQVYVVMNSVGNNCTMNFKNNNGNNIGLLGFKADTVVASTWYYTHMRD-----
 ||  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |
EEELFLPAPISDSDEFYNTIQIKEYDEQPTYSCQLFKKDEESTDEIGLIGIHRPYESGIVPEEYKDFFCIS
 340       350       360       370       380       390       400

           430       440       X
-----------HTNSNGCFWNFISEEHGWQEK
           |  |  |  |  |  |  |||
KWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
410        420       430       X

2. US-09-910-186A-14 (1-449)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score   =   158  Optimized Score  =   271  Significance =  0.58
Residue Identity =   32%  Matches         =   155  Mismatches   =   256
Gaps             =    35  Conservative Substitutions            =    35

                  X        10        20        30        40        50
                  MCESQQELNSMVTDTLNNSIPFKLSSYTDDKILISYFNKFPKRIKSSSVLMM
                  | :  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      DFDNTLKKNLLNYIDENKLYLIGSAEYESKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSELNNIILNL
        360       370       X 380       390       400       410       420
```

Copied from 10/910,186 on 05-05-2004

```
          60         70         80         90        100        110        120
RYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYD
                                                                          
          130        140        150        160        170        180        190
NKIVN--VNNEYIIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGNNANGISDTKINWIPVTITN
                                                                          
          200        210        220        230        240        250        260
DRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPN
                                                                          
          270        280        290        300        310        320        330
TNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDSTLSINNIRSTILLANRLYSGIKVKI-------QRVN
                                                                          
          340        350        360        370        380        390
NSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSG-----NREWQVVVMNSGVGNNCTMN
                                                                          
          400        410        420        430        440        X
FKNNNGNNIGLLGFKADTVVASTWYTTHMRD---------------HTNSNGCFWNFISEEHGWQEK
                                                                          
          460        470        480        490        500        510
YSNSMTENFSTSFWIRIPKYFNSI-SLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
                                                                          
          520        530        540        550        560
DLSGNIHVSDNILFKIVNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLN
                                                                          
          570        580        590        600        610        620        630
N-LNNAKIYINGKLESNTDIKDIREVIANGSIIFKLDGDIDRTQFIWMKYFSITWTELSQSNIEERYKIQSY
                                                                          
          640        650        660        670        680        690        700        710
SEYLKDFWGNPLMYNKEYYMPNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSN
                                                                          
          720        730        740        750        760        770        780
SQSINDDIVRKEDYIYLDFFNLWQEWRVYTYKYFKKEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLL
                                                                          
          790        800        810        820        830        840        850
FKKDEESTDRIGLIGIHRFYESGIVPEETYKDYFCISKWYLKEVRKRPYNLKLGCNWQFIPKDEGWTE
                                                                          
US-09-910-186A-14 (1-449)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Partial Score     =   143  Optimized Score  =   276  Significance = -1.15
Residue Identity  =   44%  Matches          =   185  Mismatches   =   192
Gaps              =    20  Conservative Substitutions            =    18

          40        50  X      60         70         80         90        100
LISYFNKFPKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYII
                          ||   :|  | ||  |  | |||   :|   : :   |  :
                          RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLPNLESSKIEVILKNAIV
                          X          10         20         30         40         50
          110        120        130        140        150        160        170
YDNKYKNFSISFWVRIPNYDNKIVNVNNEYIIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGN
|   |  | || ||||||| |  | |   |||||||:|||||||  |||||||  | |:  | |
YNSMTENFSTSFWIRIPKYFNSI-SLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
          60         70         80         90        100        110        120
          180        190        200        210        220        230        240
AMGISDYINKWIFVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKIVNCSYTRYIGIRYFNIF
          |||||:|||||||| |  || |||| ||||| | ||||| | ||:|  |  | | |||  :|||  |
MINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTNRYIWIKYFNLF
          130        140        150        160        170        180        190

250        260        270        280        290        300        310
DKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDSTLS-------INNIRST
|||| | ||  || |  |||||| || ||| ||:||  || :::
DKELNEKEIKDLYDNQSNGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTN
    200        210        220        230        240        250        260

    320        330        340        350        360        370        380
ILLANRLYSGIKVKIQRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSGNNFNQ
| |  || | |  : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
IYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ
 270        280        290        300        310        320        330
```

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          390        400        410        420        430        440
VVVMNS-----VGNNCTMNFKNNNGNNIGLLGF----KADTVVASTWYTTHMRDHTNSNGCFWNFISEEHGW
||||  |     | | | ||  |||| ||  ||          ||| |  |  |  |  |  |  || | ||
VVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFNQFNNIAKLVASNWYNRQIERSSRYLGCSWSFIPVDDGW
340        350        360        370        380        390        400        410

  X
QEK
 ||
GERPL
  X
```

Created from 10918.0 on 07 Nov 2002

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15.res made by bobryen on Thu 7 Nov 102 14:45:08-PST.


Query sequence being compared:US-09-910-186A-15 (1-1317)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-15 (1-1317) with:
          File : US08123975A.Seq
```

```
                        PARAMETERS

Similarity matrix          Unitary     K-tuple                    4
Mismatch penalty                 1     Joining penalty           30
Gap penalty                   5.00     Window size              500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                     SEARCH STATISTICS

Scores:                      Mean          Median     Standard Deviation
                              558             542                  15.01

Times:                        CPU                       Total Elapsed
                     00:00:00.00                    00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	567	777	0.60	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	567	777	0.60	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	541	675	-1.13	0

```
1. US-09-910-186A-15 (1-1317)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =   567 Optimized Score  =   777  Significance =  0.60
Residue Identity  =   60% Matches          =   813  Mismatches   =   473
Gaps              =    59 Conservative Substitutions              =     0

          10         X  20        30        40        50        60        70
GAATTCACGATGTCCTACACCAACGACAGATCCTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAG
                     ||  | | | | |  | ||| | |  |||||     |     |||||| ||||
                     CTCGAGCCATGGGCTCG--TCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATC
                     X         10        20        30        40        50

          80        90        100       110       120       130       140
GACAACTCCATCTTGGACATGAGATACGAAACAATAAGTTCATCGACACTCTCCGGTACGGTTCCAACATC
  | | |||||| || || | |||||  ||| |  | |||||  | ||  | ||| |||||| |||
AATAACCTCCATCCTGAACCTGCGCTACGAATCCATCACCTGATCGACCTGTCCGCTACGCGTCCAAAATC
  60        70        80        90        100       110       120

          150       160       170       180       190       200       210
TCCATCAACGGTGACGTCTACATCTACTCCACCAATAGAAACCAGTTCGGAATCTACTCCTCCAAGCCTTCC
  ||||     | |||  || ||  | |  | | | | |||  ||  | | |     | ||||
  AACATCGGTTCTAAAGTTAACTGCGATCGATACGACAAGAAATCAGATCCAGCTGTTCAATCTGGAATCTTCC
130       140       150       160       170       180       190       200

          220       230       240       250       260       270       280
GAGGTCAACATCGCTCAGAACAACGACATCATCTACAACGGAAGATACCAGAACTTCTCCATCTCCTTCTGG
  | | |     | ||  | | |  |||||     | ||  | |||||||||||||||||||||||||||
  AAAATCGAAGTTATCCTGAGACAATGCTATCGTATACAACTCTATGTACAAACTTCTCCACCTCCTTCTGG
            210       220       230       240       250       260       270

290       300       310       320       330       340       350       360
GTCCGTATCCCAAAGTACTTCAACAAGGTCAACCTGAATAACGAGTACACCATCATCGACTGCATCCGTAAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCACAACTGCATCGAAAAC
      280       290       300       310       320       330       340

          370       380       390       400       410       420       430
AATAACCCCGGATGGAAGATCTCCCTGAACTACAACAAGATCATCTGGACCCTGCAGGACACCGCCGGTAAC
|||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAT---TCTGGTTGGAAAGTATCTCTGAACTACGGTGAATCATCTGGACTCTGCAGGACACTCAGGAAATC
      350       360       370       380       390       400       410

          440       450       460       470       480       490       500
AATCAGAAGTTGGTCTTCAACTACACCCAGATGATCTCCATCTCCGACTACATCAACAAGTGGATCTTCGTC
|| ||||                                                              ||||
AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
      420       430       440       450       460       470       480

          510       520       530       540       550       560       570
ACCATCACCAATAACCGTTTGGGAAACTCCAGAATCTACATCAACGGTAACTTGATCGACGAGAAGTCCATC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
  490       500       510       520       530       540       550

  580       590       600       610       620       630       640
TCCAACTTGGGTGACATCCACGTCTCCGACAACATTTTGTTCAAGATCGTCGTTGTAACGACAC---CCGT
|||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
TCCAATCTGGGTAACATCCACGCTCTAATAACATCATGTTCAAACTGGACGTTGTCGTGACACTCACCGC
560       570       580       590       600       610       620

  650       660       670       680       690       700       710
TACGTCGGGATCCGTACTTACTTCAAAGTCTTCGACACTGAGTTGGGTAAGACCGAGATCCAGACCTTGACTCC
||| || |||||  ||||||||  | |||||| || ||  | | | | | | | |  |  |||||  |
```

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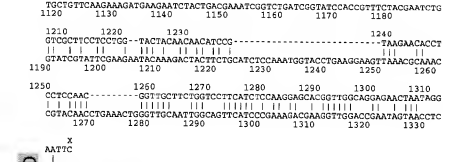
2. US-09-910-186A-15 (1-1317)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	567	Optimized Score	= 777	Significance = 0.60
Residue Identity	=	60%	Matches	= 813	Mismatches = 473
Gaps	=	59	Conservative Substitutions		= 0

Copied from 10910186 on 05-05-2004

US-09-910-186A-15 (1-1317)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 541 Optimized Score = 675 Significance = -1.13
Identity = 54% Matches = 734 Mismatches = 529
Gaps = 90 Conservative Substitutions = 0



Copied from 10910186 on 05-05-2004

Copied from 10/911,853 on 05/04/2004

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O| |O  IntelliGenetics
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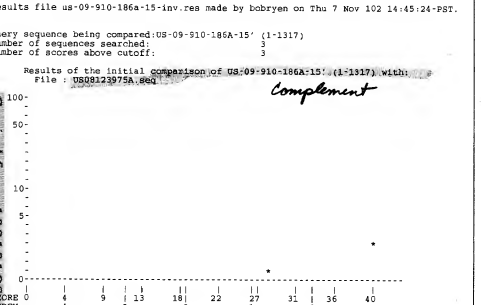
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15-inv.res made by bobryen on Thu 7 Nov 102 14:45:24-PST.

Query sequence being compared:US-09-910-186A-15' (1-1317)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-15' (1-1317) with:
        File : US08123975A.seq
```

Complement




```
                        PARAMETERS

Similarity matrix          Unitary     K-tuple                    4
Mismatch penalty             1         Joining penalty           30
Gap penalty                 5.00       Window size              500
Gap size penalty            0.33
Cutoff score                 1
Randomization group          0

                      SEARCH STATISTICS

Scores:                    Mean        Median     Standard Deviation
                             36            29          6.93

Times:                      CPU                    Total Elapsed
                      00:00:00.00                  00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	40	336	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	40	336	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	28	200	-1.15	0

```
1. US-09-910-186A-15' (1-1317)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =    40  Optimized Score  =   336  Significance =  0.58
Residue Identity =   40%  Matches          =   409  Mismatches   =   518
Gaps             =    74  Conservative Substitutions            =     0

                                X        10        20        30        40        50
                                GAATTCCTATTAGTTCTCCTCCCAACCGTGCTCCTTGGAGATGAAGGACCAG
                                ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TCTGGTTGGAAAGTATCTCGAACTACGGTGAAATCATCTGGACTCTG------CAGGACACTCAGGAAATC
  350       360       370       380       390               400       410

          60        70        80        90       100       110       120
  AAGCAAACCGTTGGAGGAGGTTGTTCTTACGGATGTTGTTGTAGTACCAGGAGGAAGCGACCAAGTTGTTGGAG
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
            420       430       440       450               460       470       480

  130       140       150       160               170       180
  TGGAAACCCAACAAACCGATGTTTCCACCGTTGTTGTCTCGAA------GTTCATGGTACAG----TTATT
  |  | | | | | | | | | | | | | | | | | | |
```

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```
  AGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGAT---CTTGTCTGC
990      1000      1010      1020      1030      1040      1050

          670       680       690       700       710       720       730
  TCCCGACGTAACGGGTGTCGTTA---CAACCGACGATCTTGAACAAAATGTTGTCGGAGACGTGGATGTCAC
  ||  ||  | |||  |  |||||   |||  |||  |||||||||||||||||||||||||||||||||||
  TCTGGAAATCCCGGACGTTGGTAATCTGTTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCAC
1060      1070      1080      1090      1100      1110      1120

          740       750       760       770       780       790       800
  --CCAAGTTGGAGATGGA-GTTCTCGTCGATCAAGTTACCGTTGATGTTATCCTGGAGTTTCCCAAACGGT
    |||| |  |||||||| |||  |||  |||  |||||||||||||||||||||||||||||||||||
  TAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAAC---GATATCGGTTTCATCGGTTTCCACCAGTT
1130      1140      1150      1160      1170      1180      1190

          810       820       830       840       850       860       870
  TATTGGTGATGGTGACGAGAATCCACTTGTTGATGATACGGAGATGGAGATCATCTGGGTGTAGTTGAAGA
  |  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AACAATATTGTAA--------ACTGGTTGCTTCCAACTGGTACAATCGTCAGATCG--AACGTTCCTCT
1200      1210      1220      1230      1240      1250

          880       890       900       910       920       930       940
  CCAACTTCTGATTGTTACCGGCGGTGTCCTGCAGGGTCCAGATGATCTTGTTGATGCTGCAGGGAGATCTTCC
  |||  ||| |||  |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
  CGCACTCTGGGTGCTCTTGGGAGT-TCATCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAAC----
1260      1270      1280      1290      1300      1310      1320

          950       960       970
  ATCCGGAGTTATTGTTACGGATGCAGTCGATGA
  |  |||  |||||||||||||||||||||||
  -CCGGGAAAGCTT
1330      X

US-09-910-186A-15' (1-1317)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    40  Optimized Score  =   336  Significance =  0.58
Residue Identity =   40%  Matches         =   409  Mismatches   =   618
Gaps             =    74  Conservative Substitutions           =     0

                    X        10        20        30        40        50
                    GAATTCCTATTAGTTCTCCTGCCAACCGTCCTCCTTGGAGATGAAGGACCAG
                    ||| | | | ||| |  | |||  | |  |||  |  ||||  ||||||||
  TCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTG------CAGGACACTCAGGAAATC
1150      1160      1170      1180      1190      1200      1210

          60        70        80        90        100       110       120
  AAGCAACCGTTGGAGGAGGTTGTCTTACGGATGTTGTTGTAGTACCAGGAGGAGCGACCAAGTTGTTGGAG
  || ||| |  |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AAACAGCTGTTCATTCAAATACCTCTCAGATCACCAACATCTCTGACTACATCAATCGCTGGATCTGTTT
     420       430       440       450       460       470       480

          130       140       150       160       170       180
  TGGAAACCCAACAAACCGATGTTCCACCGTTGTTGTCTGGAA------GTTCATGGTACAG----TTATT
  |  |  |||||||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||||
  ACCATCACCAACATCGTCTTGAATAACTCCAAAATCTACATCAACGGCCGTCGACTGACCAGAAACCGATC
    490       500       510       520       530       540       550

          190       200       210       220       230       240       250
  ACCGATGGAGTCCATGACGATGATTTGTCCCAGAGAGTTGTTAGAGTTAGAGGTACGGATCAGCTTGATGAT
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TCCAATCTGGGTAACATCCACGTCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
560       570       580       590       600       610       620

260       270       280       290       300       310       320       330
  CTTTTCAGGTTTGGCGATAGAGATATCGGCGTACAGACGGTATTCGACATCTCTGTCGACAACGTTGATGTA
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TACATCTGGATCAAATACTTCAATCTGTTCGACAAGAACTGAACGAAAAGAAATCAAAGACCTGTACGAC
630       640       650       660       670       680       690       700

          340       350       360       370       380       390
  AGCCAGATCGTTCTTTCTGAC---GAAGTTATCGGTGTTGGAAATAT-CAGTA----GATCCGTTCTTTCTG
```

```
  | |||| |  |  |  |  |||  ||  |  |  |||  |  |  |||||  |  |||  ||  |  ||
  AACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATG
          710       720       730       740       750       760       770

  400       410       420       430       440       450       460
  ATAATGACCTCGACTCCGGTGTACAATCTGGTGTTGGAGAAGATGTTTGGCTTCTGGTAGA--CACCTCTCT
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  CTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAA
    780       790       800       810       820       830       840

  470       480       490       500       510       520
  GCTGGTTGATGTTC----AAGAAGTTGGAGTTCTGGGTGATGGACTTGTCGTAC----GCAACAAGTTCAG
  |  |  |  |||    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||
  GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACGTGA-ACTCTTCCCTGTACGTGGTGCTAAATTCAT
    850       860       870       880       890       900       910

  530       540       550       560       570       580       590
  CAAGTAGTAACGTTTGT-TGTAACGACAGGTAGTTACCCCAGAAGTCCTTCTGGATGGCCGCAGGCTCGT
  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  CATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
    920       930       940       950       960       970       980

          600       610       620       630       640       650       660
  ---------CGGAGTACAAGGTCTCGATCTCGGTCTTACCCAACTCAGTGTCGAAGACTTTGAAGTAACGGA
           |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  AGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGAT---CTTGTCTGC
990       1000      1010      1020      1030      1040      1050

          670       680       690       700       710       720       730
  TCCCGACGTAACGGGTGTCGTTA---CCACCGACGATCTTGAACAAAATGTTGTCGGAGACGTGGATGTCAC
  ||  ||  | |||  |  |||||   |||  |||  |||||||||||||||||||||||||||||||||||
  TCTGGAAATCCCGGACGTTGGTAATCTGTTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCAC
1060      1070      1080      1090      1100      1110      1120

          740       750       760       770       780       790       800
  --CCAAGTTGGAGATGGA-GTTCTCGTCGATCAAGTTACCGTTGATGTTATCCTGGAGTTTCCCAAACGGT
    |||| |  |||||||| |||  |||  |||  |||||||||||||||||||||||||||||||||||
  TAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAAC---GATATCGGTTTCATCGGTTTCCACCAGTT
1130      1140      1150      1160      1170      1180      1190

          810       820       830       840       850       860       870
  TATTGGTGATGGTGACGAGAATCCACTTGTTGATGATACGGAGATGGAGATCATCTGGGTGTAGTTGAAGA
  |  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CAACAATATCGCTAA--------ACTGGTTGCTTCCAACTGGTACAATCGTCAGATCG--AACGTTCCTCT
1200      1210      1220      1230      1240      1250

          880       890       900       910       920       930       940
  CCAACTTCTGATTGTTACCGGCGGTGTCCTGCAGGGTCCAGATGATCTTGTTGATGCTGCAGGGAGATCTTCC
  |||  ||| |||  |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
  CGCACTCTGGGTTGCTCTTGGGAGT-TCATCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAAC----
1260      1270      1280      1290      1300      1310      1320

          950       960       970
  ATCCGGAGTTATTGTTACGGATGCAGTCGATGA
  |  |||  |||||||||||||||||||||||
  -CCGGGAAAGCTT
1330      X

3. US-09-910-186A-15' (1-1317)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    28  Optimized Score  =   200  Significance =  -1.15
Residue Identity =   43%  Matches         =   239  Mismatches   =   286
Gaps             =    28  Conservative Substitutions           =     0

          770       780 X     790       800       810       820       830
  AGTTACCGTTGATGTTATCCTGGAGTTTCCCAAACGGTTATTGGTGATGGTGACGAAGATCCACTTG---T
                          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |   |
                          ATGGCTTTCAACAAATACAATTCCGAAATCCGAACAATATCATCCTGAACC
                          X         10        20        30        40        50

                  840       850       860       870       880       890
```

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```
TGATGTAGTCGGAGATGGAGATCATC--TGGGTGTAGTTGAAGACCAACTTCTGATTGTTAC--CGGCGGTG
||  ||    || |  |  | |||  |  || | |||  |  | |   |||   ||| |  ||
TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
      60         70        80        90       100       110       120

900          910       920       930       940       950       960
TCCTG-----CAGGGTCCAGATGATCTTGTTGTAGTTCAGGGAGATCTTCCATCCGGAGTTATTGTTACGGA
 |||      || |  |||| |  |   ||  | |||  |  |||  |  ||||  |  |  |  |  || ||
AACTGAATGACAAGAACCAGTTCAAACTGACCT-CTTCGGCTAACTCTAAGATCCGTGTTACT-----CAGA
   130       140       150       160       170       180       190

 970          980       990      1000      1010      1020      1030
TGCAGTCGATGATGGTGTACTCGTTATTCAGGTTGACCTTGTTGAAGTACTTTGGGATACGGACCCAGAAGG
  |||   ||  ||  |  ||||  |||||    ||  |||  |    | |||  |||| || ||  ||||
ATCAGAACATCATCTTCAACTCCGTATTC---CTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAAT
       200       210       220       230       240       250

1040      1050      1060      1070      1080      1090      1100
AGATGGA-GAAGTTCTGGTATCTTCCGTTGTAGAATGATGTCGTTGTTCTGAGCGATGTTGA-CCTCGGAAGG
| | | | | | | |     | | |  ||||  |   |  | | | |  |  |  |     |  |  |
ACAAGAACCGACGGTATCCAGAAATTACATCCACAATGAAATACACCATCATCAACTGCATGAAGAATAACTCTG
260       270       280       290       300       310       320       330

1110      1120      1130      1140      1150      1160      1170
CTTGGAGGAGTAGATTCCGAACTGGTTTCTATTGGTGGAGTAGATGTAGACGTCACCGTTGATGGAGATGTT
 |||||  ||    ||||    |  |  |||| |   | ||  ||| || | |  |     |  |  |  |
GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACT-CTGATCGATATCAACGGTAAGACCAAATCT
      340       350       360       370       380       390       400

1180      1190      1200      1210      1220      1230      1240      1250
GGAACCGTAACCGGAGATGTCGATGAACTTATTGTTTCGTATCTCATGTCCAAGATGGAGTTGTCCTTGAT
| | | |  |  |  |  |  |||| |  | | |  |  ||  |||  |  | |  |  |  |  || | |
GTAATTCTTCGAATACAAACATCCGTGAAGACA-TCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCAC
      410       420       430       440       450       460       470

          1260      1270      1280      1290      1300      1310      x
C---TTCTTGTACAGCTTGTTGAAGTACAAGATCAGGATCTTGTCGTTGGTGTAGGACATCGTCAATTC
|   || |||  |  |  |  |||| | | |  |  |  |  |  |  |  |  |||||  |
CAATAACCTGAACAATGCTAAAATCTACATCAAGCGTAAACTGCAATCTAATACCGACATCAAAGACATCCG
    480       490       500       510       520       530       540 X

TGAAGTTATCGCTAACG
  550       560
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-16.res made by bobryen on Thu 7 Nov 102 14:34:47-PST.


Query sequence being compared:US-09-910-186A-16 (1-432)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-16 (1-432) with:
          File : US08123975A.pep

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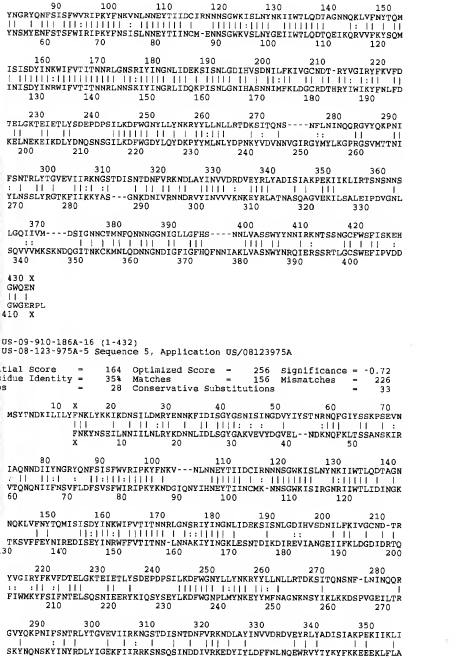
```



Copied from 10910186 on 05-05-2004

US-09-910-186A-16 (1-432)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 164 Optimized Score = 256 Significance = -0.72
Residue Identity = 35% Matches = 156 Mismatches = 226
Gaps = 28 Conservative Substitutions = 33

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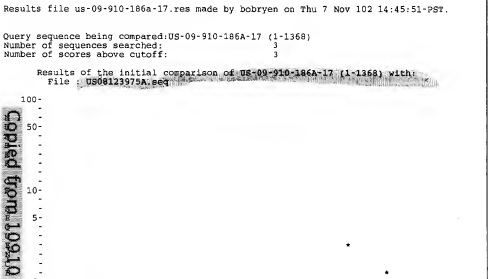
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17.res made by bobryen on Thu 7 Nov 102 14:45:51-PST.

Query sequence being compared:US-09-910-186A-17 (1-1368)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-17 (1-1368) with:
File : US08123975A.seq



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	520	499	39.26
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	566	797	1.17	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	498	706	-0.56	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	498	706	-0.56	0

1. US-09-910-186A-17 (1-1368)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score	= 566	Optimized Score	= 797	Significance	= 1.17
Residue Identity	= 613	Matches	= 699	Mismatches	= 488
Gaps	= 39	Conservative Substitutions		= 0	

```
           20        30        40        50        60        70        80
TGAAGGACACCATCCTGATCCAGGTCTTCAACAACTACATCTCCAACAGTCCCTCCAACGCCATCCTGTCCC
                                  ||  |||||||| |||| ||| | ||  |||  |||||||  ||
                          ATGGCTTTCCAACAAATACCAATTCCGAAATCTGAACAATATCATCCTGAACC
                          X         10        20        30        40        50

           90       100       110       120       130       140       150
TGTCCTACCGTGGTGGTCGTCTGATCGACTCCTCCGGTTACGGAGCCACCATGAACGTCGGTTCCGACGTCA
||  |||  |  |  |||||||||  || ||||||||| | |  |  |  |  |  |  |  |  |  |  ||
TGCGTTACCAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTCCTAAAGTTGAACTATACGACGGTGTTC
          60        70        80        90       100       110       120

       160       170       180       190       200       210       220
TCTTCAACGACATCGGTAACGGTCAGTTCAAGCTGAACAACTCCGAGAACTCCAACATCACCGCCCACCAGT
|  |||  |||  |||||||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AACTGAATGAC------AAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
   130       140       150       160       170       180       190

       230       240       250       260       270       280       290
CCAAGTTCGTCGTCTACGACTCCATGTTCGACAACCTTCCCATCAACTTCTGGGCCGTACCCAAAGTACA
  ||  | |||  |||||||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTCTGGATCCGTATCCCGAAATACA
          200       210       220       230       240       250       260

300       310       320       330       340       350       360       370
ACAACAACGACATCCAGACCTACCTCGAGAACGAGTACACCATCATCCTCCTGTATCAAGAACGACTCCGGTT
| | |||  |||  |||||||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTT
          270       280       290       300       310       320       330

           380       390       400       410       420       430       440
GGAAGGTCTCCATCAAGGTCAACCGTAATCATCTGGACCCTGATCGACGTCAACGCCAAGTCCAAGTCCATCT
|||||  |||||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GGAAGATCTCCATCCGCGGTAACGGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTAT
  340       350       360       370       380       390       400

       450       460       470       480       490       500       510
TCTTCGAGTACTCCATCAAGGACAACATCTCCGACTACATCAACAAGTGGTTCTCCATCACCATCACCAACG
|||||||  |||  ||||  ||  |||||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATA
  410       420       430       440       450       460       470

       520       530       540       550       560       570       580
ACCGCTCGGGTAACGCCAACATCTACATCAACGGTTCCTGAA---GAACTCCGAGAAGAATCCTGACCTGG
||  |||  || ||  |||||||||  |||  |  |  ||  |||  |  |  |  |  |  |  |  |  |
AC---CTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTG
480       490       500       510       520       530       540

       590       600       610       620       630       640       650
ACCGTATCAACTCCTCCAACGACATCGACTTCAAGCTGATCAACTGTACCGACACCACCAAGTTCGTCTGGA
|  |||  |  |  |  |  ||  ||||||  |||  |  |  |  |  |  |  |  |  |  |  |  |
AACTTAT---CGCTAACGGTGAAATCAGCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
550       560       570       580       590       600       610

       660       670       680       690       700       710       720
TCAAGGACTTCAACATCTTCGGTCGTGAGCTGAACGCCACCGAGGTCTCCTCCCTGTACTGGATCCAGTCCT
```

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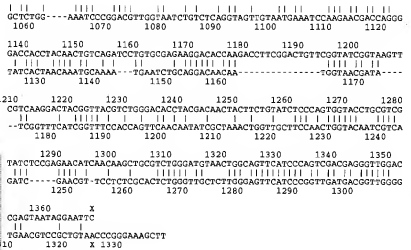
2. US-09-910-186A-17 (1-1368)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	498	Optimized Score	= 706	Significance = -0.56
Residue Identity	=	54%	Matches	= 758	Mismatches = 551
Gaps	=	70	Conservative Substitutions	=	0

Copied from 10910186 on 05/05/2004



Copied from 10910186 on 05-05-2004

Copied from 10914186 on 05/13/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17-inv.res made by bobryen on Thu 7 Nov 102 14:46:08-PST.

Query sequence being compared:US-09-910-186A-17' (1-1368)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-17' (1-1368) with:
          File : US08123975A.seq                    complement

 100 -
     -
     -
  50 -
     -
     -
     -
     -
  10 -
     -
   5 -
     -
     -
   0 ----------------------------------------------------------------------
     |    |    |    |    |    |    |    |    |    |    |    |    |    |
SCORE 0|    4    |8   12   | 16   20   | 24   28|   32   36
DEV -4          -3        -2        -1         0

                              PARAMETERS

Similarity matrix      Unitary      K-tuple                        4
Mismatch penalty             1      Joining penalty               30
Gap penalty               5.00      Window size                  500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                  Mean          Median      Standard Deviation
                           32              25                    6.93

Times:                    CPU                       Total Elapsed
                  00:00:00.00                    00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	36	464	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	36	464	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	24	52	-1.15	0

```
1. US-09-910-186A-17' (1-1368)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =    36  Optimized Score  =   464  Significance =  0.58
Residue Identity =   40%  Matches          =   563  Mismatches   =   708
Gaps             =   108  Conservative Substitutions             =     0

                        X        10        20        30        40        50
                        GAATTC--CTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGT
                        ||||||  |  ||    ||  ||||  ||||||||||||||||||||||||||
  GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAAT
     20        30     X  40        50        60        70        80

     60        70        80        90       100       110
  TACATC-CCAGACGCAGCT-TGTTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGAT----ACAGA
  ||| || | | |  |||| | |  ||  |||| | | |  |||| | | |  |||| | | |    ||||
  CCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
   90       100       110       120       130       140       150

    120       130       140       150       160       170       180
  AGTAGTTGTCGTAGGTGTCCAGACGTAACCGTAGTCCTTGACGAACTTACCGATACCGACAGTCCGAAGG
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  TCGACAAGAATCAGATCCAGCTGGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCG
160       170       180       190       200       210       220       230

  190       200       210       220       230       240       250       260
  TCTTGGTGTCCTTCTCGCACAGGATCGACAGTTGTAGGTGGTCTTCTCGTAGTACTTCTGTACGTGCAGGA
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  TATACAACTCTATGTACGAAAACTCTCTCCACCTCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCT
   240       250       260       270       280       290       300

    270       280       290       300       310       320
  CGTCGTAGAAGGTAGGTGGTCGTTGATTGGGGCCAGGAAACAGCTGGGTCTGA---TCTCCTTGGAGT---
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  CTCTGCAACATGAATACACCATCACTGCATGGAAACAATTCTGGTTGGAAACTATCTCTGAACTACG
   310       320       330       340       350       360       370

   330       340       350       360       370       380       390
  TGACCAGGACGTAGACACGGTAGGACTCGTCGGAGATGTTGTCGATGTTCAGGTAGATGTAGTCACCCTCAC
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  GTGAAATCATCTGGACTCTGCAGGACACTCAGCATAAT--------CAAACGCGTGTTGTACTTCAAATACTC
   380       390       400       410       420       430

  400       410       420       430       440       450       460
  GGACGATGTTGTCGTTGTTGATGTTACGGGAGTTGGAGC-CCTTCTTGATGATGAAACGCAGACCCAGGTAC
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  TCAGATGTCAACATCTCTGA--CTACATCAATCGCTGGATCCTCGTACCACATCACCAACAATCGTCTGAAT
440       450       460       470       480       490       500

  470       480       490       500       510       520       530       540
  AGGTTCTGGTAGTTGATGGCGGCGTTGTTGAAGTTGGTACGAGGGGCGGTCTCACCCATGGAGGCCTTGGAG
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  AACTCCAAAATCTACATCAACGGCCGTCCTCA---TCGACCAGAAACCGAATCCTCAATCTGGGTAACATCCA-
510       520       530       540       550       560       570

         550       560       570       580       590       600       610
  AAGTACTTGAATGTAGATGTTCTGCATACCCTGGTTGAACAGGTAGTACTGGGTGTCGTAACGCAGTGGGTTT
  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |  | | |  |
  ------------CGCCTCTAATAACATCATGTTCAAACTGG------ACGGTTGTCGTGACACTCACCGCTA
              580       590       600       610       620       630

         620       630       640       650       660       670       680
  CCCCAG----AAGTCCTTCAGGGTGTT-GGTGGAGGACTGGATCCAGTACAGGGAGGAGACCTCGGTGGCGT
  |  | |    || | |||||  |||| |  | | |  |  | | |  |  | | |  |  |||||  | |
```

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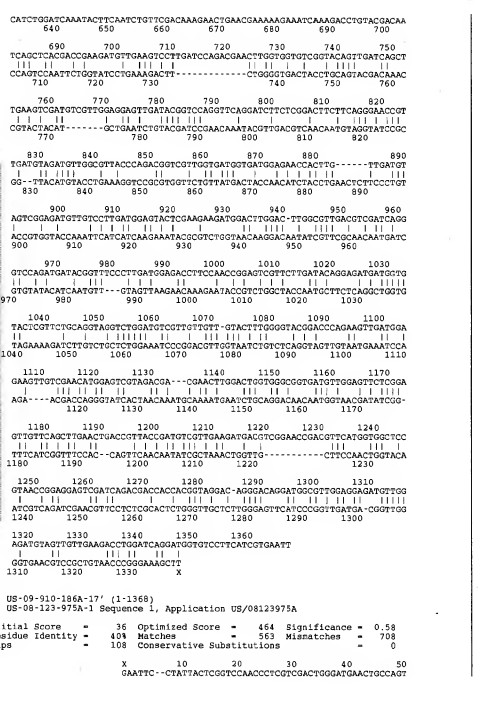

2. US-09-910-186A-17' (1-1368)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	36	Optimized Score	=	464	Significance = 0.58
Residue Identity	=	40%	Matches	=	563	Mismatches = 708
Gaps	=	108	Conservative Substitutions	=		0

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```
GG--TTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGT
  830       840       850       860       870       880       890

          900       910       920       930       940       950       960
AGTCGGAGATGTTGTCCTTGATGGAGTACTCGAAGAAAGATGGACTTGGAC-TTGGCGTTGACGTCGATCAGG
|   |   |   | | | || || |   |   |     |   |||| |  |||| |  | | ||
ACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATC
900       910       920       930       940       950       960

      970       980       990      1000      1010      1020      1030
GTCCAGAGTATACGGTTTCCCTTGATGGAGACCTTCCAACCGGAGTCGTTCTTGATACAGGAGATGATGTG
|| | |   | |||   | | |     ||      | | | | |  | |  | | |||||
GTGTATACATCAATGTT---GTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTG
970       980       990      1000      1010      1020      1030

     1040      1050      1060      1070      1080      1090      1100
TACTCGGTTCTGCAGGTAGGTCTGGAGTGTCGTTGTTGTT-GTACTTTGGGGTACCGGAACCAGAAGTTGATGGA
||          |   | |||||  ||   |  ||| ||| | ||   | | |  ||   || |
TAGAAAAGATCTTGTCTGCTCTGGAAATCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCA
1040      1050      1060      1070      1080      1090      1100      1110

     1110      1120      1130      1140      1150      1160      1170
GAAGTTGTCGAACATGGAGTCGTAGACGA---CGAACTTGGACTGGTGGGCGGTGATGTTGGAGTTCTCGGA
   |   ||| || ||  ||   || |  | | | |  ||| || | |  |||  | | | ||||
AGA----ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACATGGTAACGATATCGG-
          1120      1130      1140      1150      1160      1170

     1180      1190      1200      1210      1220      1230      1240
GTTGTTCAGCTTGAACTGACCGTTACCGATGTCGTTGAAGATGACGTCGGAACCGACGTTCATGGTGGCTCC
|| || | ||  ||    | | | || ||| | ||   |  |          |||   ||| |
TTTCATCGGTTTCCAC--CAGTTCCAACAATATCGCTAACTGGTTG----------CTTCCAACTGGTACA
1180      1190      1200      1210      1220              1230

 1250      1260      1270      1280      1290      1300      1310
GTAACCGGAGGAGTCGATCAGACGACCACCACGGTAGGAC-AGGGACAGGATGGCGTTGGAGGAGATGTTGG
|  | |||     || ||   |  |  |  |||  |  ||||    || | | || ||  ||||
ATCGTCAAGTCGAAGGTTCCTCTCCCACTCTGGGTGCTCTGGGAGTCATCCCGGTTGATGA-CGGTTGG
1240      1250      1260      1270      1280      1290      1300

1320      1330      1340      1350      1360
AGATGTAGTTGTTGAAGACCTGGATCAGGATGGTGTCCTTCATCGTGAATT
  |||  |||| |  |||  |||
GGTGAACGTCCGCTGTAACCCGGGAAAGCTT
1310      1320      1330      X

US-09-910-186A-17' (1-1368)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    24  Optimized Score  =    52  Significance = -1.15
Residue Identity =   42% Matches          =    68  Mismatches   =   81
Gaps             =    10  Conservative Substitutions =     0

                   X       10        20        30        40        50
                   GAATTCCTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGTTA
                   | | | | |  |||  |  ||  | | ||| |  |  |  | | |||||
GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTC--TGCATCTCCAAATGGTACCTGAAGGAAGTTA
    1190      1200  X  1210      1220      1230      1240      1250

       60        70        80        90       100       110       120
CATCCCAGACGCAGCTTGTTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGATACAGAAGTAGTTG
  |  | | |  |  |  |  |  |  |  |  |||| |  ||  | | | | | | | | | | |
AACGCAAACCGTACAACCTGAA---ACTGGGTTGCAATTGGCAGTT--CATCCGAAAGACGAAGGTTG--G
    1260      1270      1280      1290      1300      1310

   130       140       150       X         170
TCGTAGGTGTCCCAGACGTAACCGTAGTCCTTGACGAACTTACCGATACCGAACA
  |  | | |  |  |  |  |  ||| |||  |  |  |  |  |  |  |
ACCGAATAGTAACCTCTAGAGTCG-AGGCCTGCAG
1320      1330      1340      1350
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-18.res made by bobryen on Thu 7 Nov 102 14:35:06-PST.


Query sequence being compared:US-09-910-186A-18 (1-449)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-18 (1-449) with:
        File : US08123975A.pep

 100-
    -
    -
    -
    -
  50-
    -
    -
    -
    -
    -
  10-
    -
    -
    -
    -
   5-
    -
    -
    -
    -
    -
   0-
     |    |    |    |    |    |    |    |    |    |    |
SCORE 0   23   46   69   92   115  138  161  184  207
DEV                                                -9


                        PARAMETERS

Similarity matrix       PAM-150     K-tuple                    1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty           20
Gap penalty               5.00     Window size              432
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0


                    SEARCH STATISTICS

Scores:                    Mean      Median    Standard Deviation
                            206         207                  0.58

Times:                      CPU                  Total Elapsed
                   00:00:00.00                   00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-5	Sequence 5, Application U	439	207	319	1.73	0
2. US-08-123-975A-2	Sequence 2, Application U	850	207	326	1.73	0
	**** 0 standard deviation from mean ****					
3. US-08-123-975A-3	Sequence 3, Application U	415	206	262	0.00	0

```
1. US-09-910-186A-18 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   207  Optimized Score  =   319  Significance =  1.73
Residue Identity =   49%  Matches          =   220  Mismatches   =   182
Gaps             =     9  Conservative Substitutions             =    33

          10        20        30        40        50        60        70
MKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFNDIGNGQPKLNSSENSNITAHQ
                                                                        |
                                                                        |
                                                                        |
```

Copied from 10/910,186 on 05-05-2004

US-09-910-186A-18 (1-449)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score = 205 Optimized Score = 262 Significance = 0.00
Residue Identity = 35% Matches = 151 Mismatches = 232
Gaps = 12 Conservative Substitutions = 29

Copied from 10914186 on 05/14/2004

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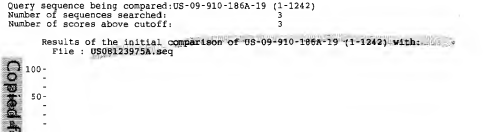
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19.res made by bobryen on Thu 7 Nov 102 14:46:34-PST.


Query sequence being compared:US-09-910-186A-19 (1-1242)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

          Results of the initial comparison of US-09-910-186A-19 (1-1242) with:
               File : US09123975A.seq
```




```
                              PARAMETERS

Similarity matrix          Unitary      K-tuple                      4
Mismatch penalty                1      Joining penalty             30
Gap penalty                  5.00      Window size                500
Gap size penalty             0.33
Cutoff score                    1
Randomization group             0

                           SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            106           100                    6.35

Times:                      CPU                     Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                          Init.  Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338   110   448  0.63   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338   110   448  0.63   0
                    **** 1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351    99   477 -1.10   0


1. US-09-910-186A-19 (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   -   110  Optimized Score  -   448  Significance =  0.63
Residue Identity -  43%  Matches         -   546  Mismatches   =   580
Gaps             -   133  Conservative Substitutions           =     0

                                x      10        20        30        40        50
                                   ATGGCTCTGAA--CGACCTGTGCATCAAAGTTAACAACTGGGACCTGTTCTT
                                   |||| || ||||  |||| | |||| | |||| |||| |||| |||| ||
                    CCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTT---AACTTCGATCCGATCGA
                       100       110   x  120       130       140       150       160

                            60        70        80        90       100       110
                    CTCCCCGTCTGAAGACAACTTCACTAACGACCTGAACAAAGGCGAAGAAATCACCTCCGACACTAACAT---
                    |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||
                    CAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATA
                       170       180       190       200       210       220       230

                  120       130       140       150       160       170       180
                    CGAAGCTGCTGAAGAAAACATCTC--------TCTGGA-CCTGATCCAGCAGTACTACCTGACCTTCAACTT
                    | || ||| | |||||| ||||        |||||| || |||| | |||| | |||| | |||| ||||
                    CAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCT
                       240       250       260       270       280       290       300

                            190       200       210       220       230       240
                    CGACCAACCGA---CCGGAAAACATCTCCATCGAAAACCTGTCT-TCCGACATCATCGGTCAGCC----GGA
                    |||| |||   |  || || |||| ||||||||  |||  | || | |||  | || |  ||||    |||
                    GAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGSTTGGAAAGTATCTCTGAACTACGGTGA
                    310       320       330       340       350       360       370

                       250       260       270       280       290       300
                    ACTGATGCCGAACATCGAACGCTTCCGAACGGCAAGAAATACGAACTGGACAAATA-----------CAC
                    | || ||    |  | |  | |  | |||  |  | |  | ||||||           ||
                    AATCATCTGGACTCTGCAGGACACTCAGGAATAAACAAACAGCGTTGTATCTAAATACTCTCAGATGATCAA
                  380       390       400       410       420       430       440       450

                       310       320       330       340       350       360       370
                    CATGTTCCACTACCT----GCGTGCTCAGGAATCGAACACGGTAAATC-TCGTATCGCTCTGACTAACTC
                    ||| | |||||  |    |||  |  |  |  |||||  |||| |  |||| |  |  |  |  |  ||
                    CATCTCTGACTACACAATCGCTGGATCTTGTTACCATCACCAACAATCGTCTGAATAACTCCAAATCTA
                       460       470       480       490       500       510       520

                             380       390       400       410       420
                    CGTTAACGAAGCTCTGCTGAACCCGTCTCGCGTTTAC---------ACCTTCTTCTCTTCCGACTAC------
                    | | ||||   |||| | ||||  | | | | | |         |||| | |||| | |||| |||||
                    CATCAACGGCCGTCTGATCGACCAGAAACGAGTCCTCAATCTGGGTAACATCCACGCTTCTAATAACATCAT
                       530       540       550       560       570       580       590

                                   430       440       450       460       470       480
                    ---------------GTTAAGAAAGTTAACAAAGCTACTGAAGCTGCTATGTTCCTGGGTTGG--GTTGA
                                   || |||| | |||| |||| |||| |||| |||| |||| |||| ||  ||||
                    GTTCAAACTGGACGGTTGTCGTGACACTCGCTACATCTGAAATCTTCAATCTGTCGACAAAGA
                      600       610       620       630       640       650       660

                            490       500               510       520       530       540
                    ACAGCTGGTTTACGACTTCACCGAC-------GAAACTTCTGAAGTTTCCACCACTGACAAAATCGCTGACA
                    ||| | |  |||| |||  |||       |||| | |  |||| | |||| |  |||  |||| |||| |||
                    ACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGG
                    670       680       690       700       710       720       730

                    550       560       570       580       590       600       610
                    TCACTATCATCATCCCGTACATCGGCCCGGCTCTGAACATCGGTAACATGCTGTACAAAGACGACTTCGT--
                    | |||| |  ||  ||  | | |  |  |  |  |||  |||  | | | |||||  |||       |||
```

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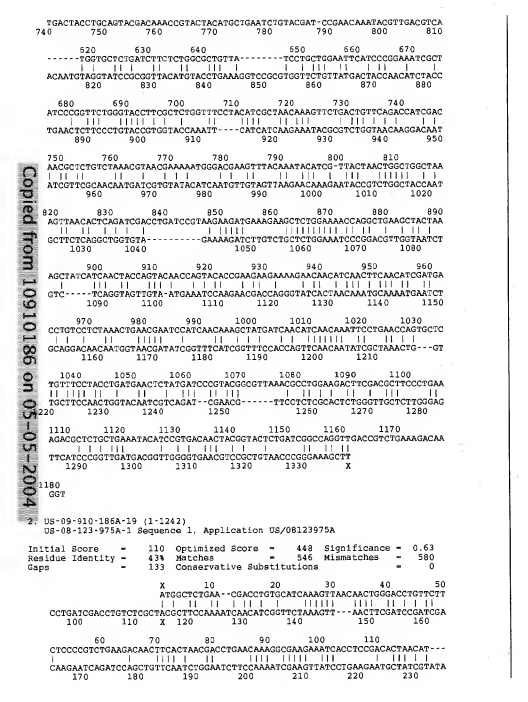

2 US-09-910-186A-19 (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 110 Optimized Score = 448 Significance = 0.63
Residue Identity = 43% Matches = 546 Mismatches = 580
Gaps = 133 Conservative Substitutions = 0

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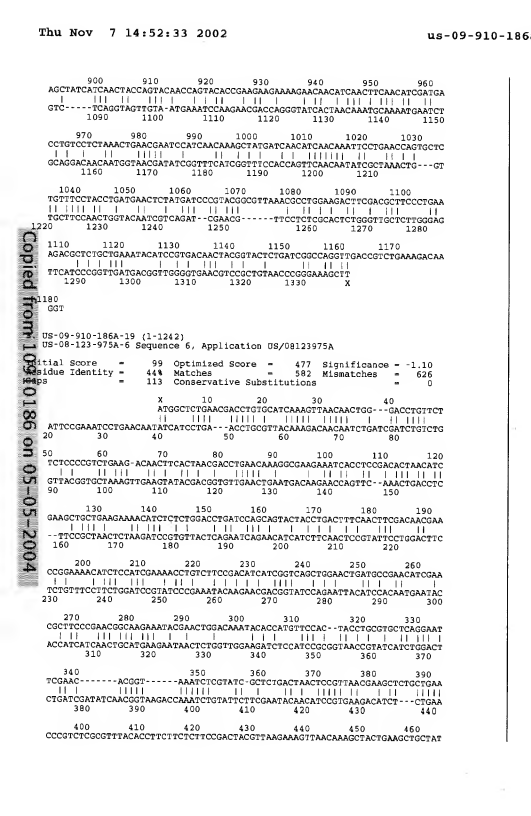

US-09-910-186A-19 (1-1242)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Partial Score = 99 Optimized Score = 477 Significance = -1.10
Residue Identity = 44% Matches = 582 Mismatches = 626
Gaps = 113 Conservative Substitutions = 0

```
TGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCC
    1290       1300       1310       1320       1330       1340
```

Copied from 10910186 on 05-05-2004

Copied from 10916186 on 05/20/2004

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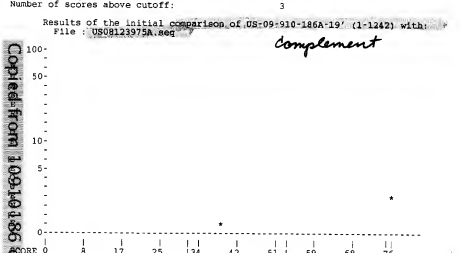
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19-inv.res made by bobryen on Thu 7 Nov 102 14:46:49-PST.

Query sequence being compared:US-09-910-186A-19' (1-1242)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-19' (1-1242) with:
        File : USO8123975A.seq
```

Complement



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	63	39	21.94

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

```
Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	76	209	0.59	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	76	209	0.59	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	38	442	-1.14	0

1. US-09-910-186A-19' (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score  =   76  Optimized Score  =   209  Significance =  0.59
Residue Identity =  39% Matches         =   248  Mismatches   =   332
Gaps           =   48  Conservative Substitutions =             =     0

  640       650       660       670       680       690       700       710
  TGTACAGCATGTTACCGATGTTCAGAGCCGGGCCGATGTACGGGATGATGATAGTGATGTCAGCGATTTTGT
                                  | | | | | | | | | | | | | | | | | | | | | |
                                  CTCGAGCCATGGCTCGTCTGCTGTCTACCTCACTGAATACATCAAGAACAT
                                  X         10        20        30        40        50

          720       730       740       750       760       770
  CAGTGGTGGAAACTTCAGAAGTTTCGTCGGTGAAGTCGTAAACCAGCTGTTCAACCCAACCCAGGA------
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CATCAAT---ACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCCGACCTGTCTCGCTACGCTTC
            60        70        80        90        100       110       120

   780       790       800       810       820       830       840
  ACATAGCAGCTTCAGTAGCTTTGTTAACTTTCTTAACGTAGTC--GGAAGAGAAGAAGGTGTAAACGCGAGA
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAAGAATCAGATCCAGCTGTTCAATCTGGA
        130       140       150       160       170       180       190

   850       860       870                 880       890       900
  CGGGTTCAGCAGAG----CTTCGTTAACGGAGTTA------------GTCAGAGCGATACGAGATTTACCGT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTC
      200       210       220       230       240       250       260

   910       920       930       940       950       960
  GTTCGAATTCCTGAGCAAGCAGGTAGTGGAACATGGTGTATTTGTCCAGTTCGTATTTCTT-----GCCGTT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CTTCTGGATCCGTATCCG-AAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCA
      270       280       290       300       310       320       330

 970       980       990      1000      1010      1020      1030
  CGGGAAGCGTTCGATGTTCGGCATCAGTCCAGCTGAC--CGATGATCTCGGAAGACAGGTTTTCGATGGAG
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  TGGAAAACAATTCTCGTTGGAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGG
      340       350       360       370       380       390       400

1040      1050      1060      1070      1080      1090      1100
  ATGTTTTCCGGTTCGTTG----------TCGAAGTTGAAAGTCAGGTAGTACTGCTGATCAGGTCCAGAC
  | | | | | ||||          || || ||| || | | ||| | | | | | | | | | | | |
  AAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA--ATCGCTGGAT
410       420       430       440       450       460       470

          1110      1120      1130      1140      1150      1160      1170
  AGATGTTTTCTTCAGCAGCTTCGATGTTAGTGTCGGAGGTGATTCCTTCCCCTTTGTTCAGGTCGTTAGTGA
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  CTTCGTTACCATCACCAACAATCGTCTCGAATAACTCCAAAATCTACATCACGGCCGTCGATCGACCAGAA
480       490       500       510       520       530       540       550

      1180      1190      1200      1210      1220      1230      1240 X
  AGTTGTCTTCAGACGGGCAGAAGAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCAT
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  ACCGATCTCCAATCTGGGTAACATCCAGCGTTCTAATAACATCATGTTCAAACTGGACGCGTTGTCGTCGACAC
      560       570       580       590       600       610       620

  TCACCGCTACATCTGGAT
      630       640
```

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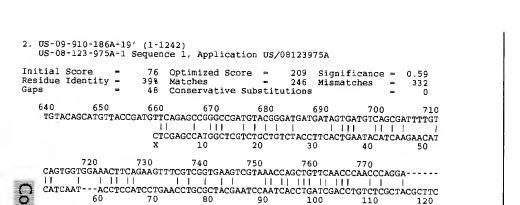
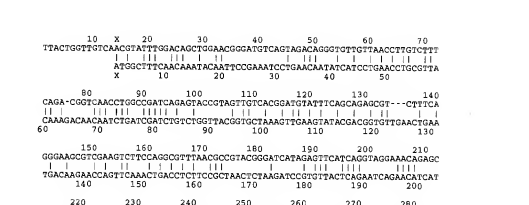
2. US-09-910-186A-19' (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

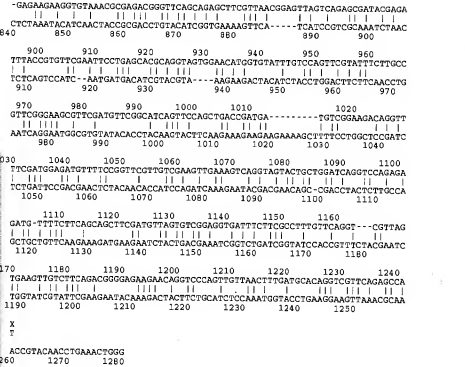
Initial Score = 76 Optimized Score = 209 Significance = 0.59
Residue Identity = 39% Matches = 246 Mismatches = 332
Gaps = 48 Conservative Substitutions = 0



3. US-09-910-186A-19' (1-1242)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 38 Optimized Score = 442 Significance = -1.14
Residue Identity = 40% Matches = 524 Mismatches = 681
Gaps = 79 Conservative Substitutions = 0





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Copied from 10510186 on 05/20/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-20.res made by bobryen on Thu 7 Nov 102 14:35:30-PST.


Query sequence being compared:US-09-910-186A-20 (1-413)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-20 (1-413) with:
          File : US08123975A.pep )
```

```
                              PARAMETERS

Similarity matrix          PAM-150      K-tuple                        1
Threshold level of sim.      16%
Mismatch penalty               1      Joining penalty               20
Gap penalty                 5.00      Window size                  413
Gap size penalty            0.05
Cutoff score                   1
Randomization group            0

                           SEARCH STATISTICS

Scores:                      Mean        Median      Standard Deviation
                               97            17              140.59

Times:                        CPU                       Total Elapsed
                      00:00:00.00                    00:00:00.00

Number of residues:                1704
Number of sequences searched:         3
Number of scores above cutoff:        3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	260	297	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	17	181	-0.57	0
3. US-08-123-975A-5	Sequence 5, Application U	439	15	179	-0.58	0

1. US-09-910-186A-20 (1-413)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score    =   260  Optimized Score  =   297  Significance =  1.16
Residue Identity =   45%  Matches         =   189  Mismatches   =   198
Gaps             =     5  Conservative Substitutions =                19

       X      10        20        30        40        50        60        70
MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEETSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIEN
                 ||| |  ||||         || | | | |         |         |  |
   APGICIDVNEDLFFIADKNSPSDDLSKNERIEYNTQSNYIENDFPINE-----LILDTDLISKIELPSE
   X      10        20        30        40        50        60

       80        90       100       110       120       130       140
LSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFSSDYV
                 | |:  | |||   | | | ||:|  |       ||| |  :|||   :|| |||  ||:
NTESLTDFNVDVPVYSEQPAIKKIFTDENTIPQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
    70        80        90       100       110       120       130

      150       160       170       180       190       200       210
KKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVI
|  || |||:|| ||| | | ||| |  |  |  |||||  |:|||| ||:|||  |  |  |  :|| |
KTANVVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
140       150       160       170       180       190       200

      220       230       240       250       260       270       280
LLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVFKYIVTNWLAKVNTQIDLIRKKMKEA
|||||||  ||| | |  |||  |||  | :|||||| |||||  | :|  |:|| ||||   |:   | |
LLEFIPELIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
210       220       230       240       250       260       270       280

      290       300       310       320       330       340       350       360
LENQAEATKAIINYQYNQYTEEEKNNIWFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPYGVKR
|  ||:|  |  || |  |  |||  |||  |  |  |  |||  |  |  |  |  |  |  |||  :| :
LNYQAQALEEIIKYRYNIYSEEKESNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVER
          290       300       310       320       330       340       350

      370       380       390       400       410  X
LEDFDASLKDALLKYIRDHYGTLIGQVDRLKDEVNNTLSTDIPFQLSKYVDNQ
|  |||  |  |||  |  |  |  |  |  |  |  |  |  |  |  |  |
LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDYILIEMFNKYNSEILNNIIL
    360       370       380       390       400  X 410       420

N
```

2. US-09-910-186A-20 (1-413)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score    =    17  Optimized Score  =   181  Significance = -0.57
Residue Identity =    9%  Matches         =    41  Mismatches   =   342
Gaps             =     5  Conservative Substitutions =                25

       X      10        20        30        40        50        60
   MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEETSDTNIEAAEENISLDLIQQYYLTFNFDNEPENI
                 | ||                |  |  |  |  |  |  |  |  |  |  |
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
   X  10        20        30        40        50        60        70

       80        90       100       110       120       130       140
SIENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFS
```

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```
                                                
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Copied from 10/910,186 on 05/13/2004

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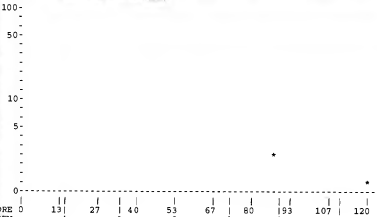
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21.res made by bobryen on Thu 7 Nov 102 14:47:13-PST.

Query sequence being compared:US-09-910-186A-21 (1-1242)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-21 (1-1242) with:
          File = US08123975A.seq
```




```
                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                    SEARCH STATISTICS

Scores:                     Mean        Median     Standard Deviation
                              98            89                  18.48

Times:                       CPU                    Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                        4027
Number of sequences searched:                 3
Number of scores above cutoff:                3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score Score	Sig.	Frame
	**** 1 standard deviation above mean ****				
1. US-08-123-975A-6	Sequence 6, Application U	1351	120 320	1.19	0
	**** 0 standard deviation from mean ****				
2. US-08-123-975A-4	Sequence 4, Application U	1338	88 394	-0.54	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	88 394	-0.54	0

```
1. US-09-910-186A-21 (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =   120  Optimized Score  =   320  Significance =  1.19
Residue Identity  =   40%  Matches         =   359  Mismatches   =   486
Gaps              =    46  Conservative Substitutions           =     0

                      X        10        20        30        40
                ATGGCTGCCAGGAATCTG--------TATCGACGTCGACAACAGGACTTGTT
                                  |  |||  ||  |||  |  |  |||||  | ||
     CAATCGCTGGTTCTTCGTTACCATCACCAATAACTGAACAATGCTAAAATCTACATCAACGGTAAACTGGA
      450       460       470       480       490       500       510

          50        60        70        80        90       100       110
     CTTCATATCGCTGACAAGAACTCCTTCTCCGACGACTTGTCCAAGAACGAGAGAA---TCGAGTACAACACCCA
      |  |   | ||||     |  |  ||  | |  |  |  |  |  |  |  |   |  |  |  |  |  |
     ATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGA
    520       530       540       550       560       570       580       590

         120       130       140       150       160       170       180
     GTCCAACTACATCGAGAACGACTTCCCAATCAACGAGTTGATCTTGGACACCGACTTG---ATCTCCAAGAT
      | |   | |  |  |  |     |  |  |  |||||  |||||||  ||     |||||  ||
     CATCGATCGTACCCAGTCCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATAT
          600       610       620       630       640       650       660

              190       200       210       220       230       240
     CGAGTTGCCATCCGAGA---------ACACCGAGTCCTTGACTGACTTCAACGTCGACGTCCCAGTCTACGA
     |||  |  |  | |||         |||||  | | |||  |||||  |  |  |  |  |  |  | | ||
     CGAAGACGGTACAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAA
          670       680       690       700       710       720       730

          250       260       270       280       290       300       310
     GAAGCAACCAGCTATCAAGAAGATTTTCACCGACGAGAACACCATCTTCAATACCTGTACTCTCAGACCTT
      ||  |||   |||  |  |  |  |  |  |  |  |||  |  |  |  |  |  |  |||||  |
     CAAAGAATACTATATGTTCAATGCTGGTGATAACAAGAACTCTTACAAGTCAAACTGAAGAAAGACTCTCGGTTGG
        740       750       760       770       780       790       800

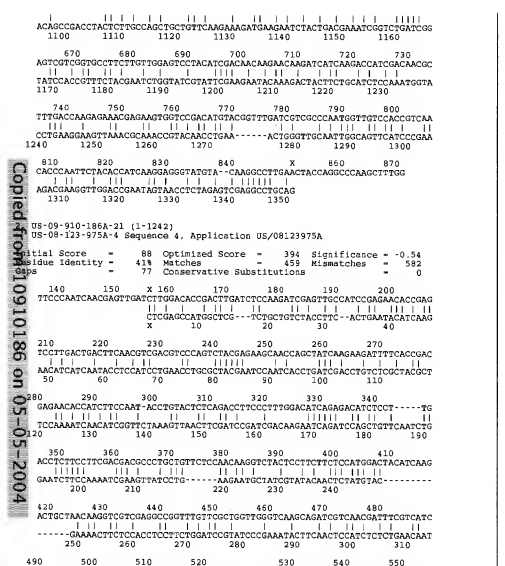
     320       330       340       350       360       370       380
     CCCTTTGGACATCAGAGACA---TCTCCTTGACCTCTTCCTTCGACGACGCCCTGCTGTTCTCCAACAAGGT
      |  |  |  |  |  |||   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
     TGAAACCTGACTCGTTCCAATACAACCAGAACTCTAAATACACATCAACTACCCGACCTGCTACATCGGTGA
      810       820       830       840       850       860       870

      390       400       410       420       430       440       450
     CTACTCCTTCTTCTCCATGGACTACATCAAGACTGCTAACAAGGTCGTCGAGGCCGGTTTGTTCGCTGGTTG
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
     AAAGTTCATCACTGCGTCGCAAACTAACTCTCAGTCCACCAATGATGACATCGTACGTAAAGAAGACTACAT
     880       890       900       910       920       930       940       950

     460       470       480       490       500       510       520
     GGTCAAGCAGATCGTCAAC--GATTTCGTCATCGAGGCTA-ACAAGTCCAACACCATGGACAAGATTGCCGA
      |  |  |  |  |  |||   |  |  |  |  |  | | |  |  |  |  |  |  |  |  |  |  |
     CTACCTGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGA
             960       970       980       990      1000      1010      1020

     530       540       550       560       570       580       590
     CATCTCCTTGATTGTCCCATACATCGGTTTGGCCTTGAACGTCGGTAACGAGACCGCCAAGGGTAACTTCGA
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
     AAAGCTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGA
         1030      1040      1050      1060      1070      1080      1090

     600
      GAA-------CGCTTTCGAGATCGCTGGTGCCTCCATCTTGTTGGAGTTCATCCCAGAGTTG--TGATCCC
```



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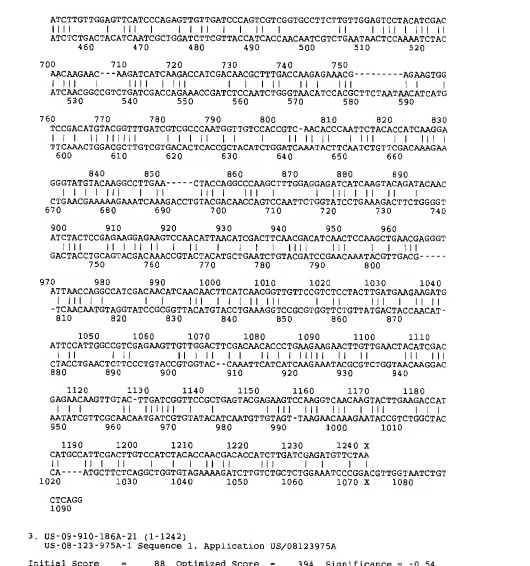
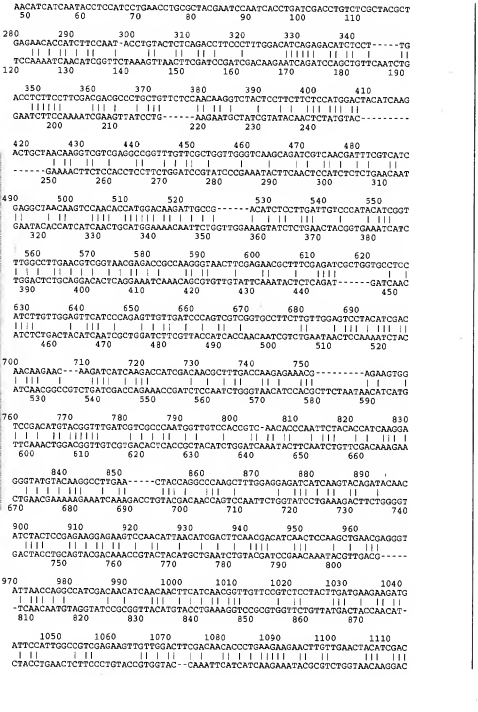
US-09-910-186A-21 (1-1242)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 88 Optimized Score = 394 Significance = -0.54
Residue Identity = 41% Matches = 459 Mismatches = 582
Gaps = 77 Conservative Substitutions = 0



3. US-09-910-186A-21 (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 88 Optimized Score = 394 Significance = -0.54
Residue Identity = 41% Matches = 459 Mismatches = 582
Gaps = 77 Conservative Substitutions = 0



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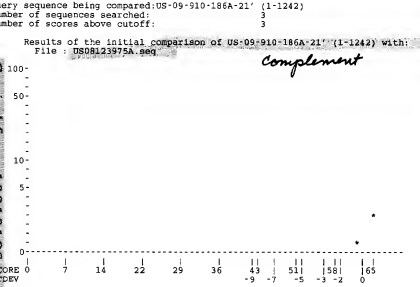
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21-inv.res made by bobryen on Thu 7 Nov 102 14:47:31-PST.

Query sequence being compared:US-09-910-186A-21' (1-1242)
Number of sequences searched:                3
Number of scores above cutoff:               3

        Results of the initial comparison of US-09-910-186A-21' (1-1242) with:
            File - US08123975A.seq
```

Complement



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	63	62	2.31

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

```
Number of residues:                4027
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	65	457	0.87	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	65	457	0.87	0
3. US-08-123-975A-6	Sequence 6, Application U	1351	61	448	-0.87	0

1. US-09-910-186A-21' (1-1242)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	= 65	Optimized Score	= 457	Significance	= 0.87
Residue Identity	= 424	Matches	= 556	Mismatches	= 657
Gaps	= 108	Conservative Substitutions			= 0

```
                    X       10        20        30        40
                    TTAGAACATCTCGATCAAGATGGTGTCGTTGGTGTAGATG---GACAAGTCG
                    || | ||  ||||  |  ||  || ||  ||  ||  ||| | ||
                    CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGACCTGCGCTACAATCC
                      20        30        40        50        60        70        80

          50        60        70        80        90       100                 110
          AATGGCATGATGG---TCTTCAAGTACTTGTTGACCTTGGACTTTGCTACTCAG------CGGAACCGATC
          ||| | ||||| |   |  |  ||||  |  |  ||  ||  |  ||  ||  |      ||| ||||||
          AATCACCTGATCGACCTTCCTCGCTACGCTTCCAAAATCAACATCGGTCTAAAGTTAACTTCGATCCGATC
        90        100       110       120       130       140       150       160

                  120       130       140                 150       160
          AAGTACAACTTGTTCTCGTCGATGTAGTTCAA------------CAAGTTCTTCTTCAGGGTGTTGTCG--
                | | |||  |  |  |  ||  |||            |||| | ||| | ||  ||| |||
          GACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTA
                170       180       190       200       210       220       230

                  170       180       190       200                 210
          ---------AAGTCCAACAACTTCCGACGGCCAATGGAAT---------------CATCTTCTTCATCAAG
                   |||  |  |  ||  |  |  ||  |||||               |||  |||  |||
          TACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
                240       250       260       270       280       290       300

          220       230       240       250       260       270       280
          TAGGAGACGGAACAACCGTTGATGAAGTTGTTGATGTTGTCGATGGCCTGGTTAATACCCTCGTTCAGCTTG
          || | ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||
          CTGACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGT
            310       320       330       340       350       360       370

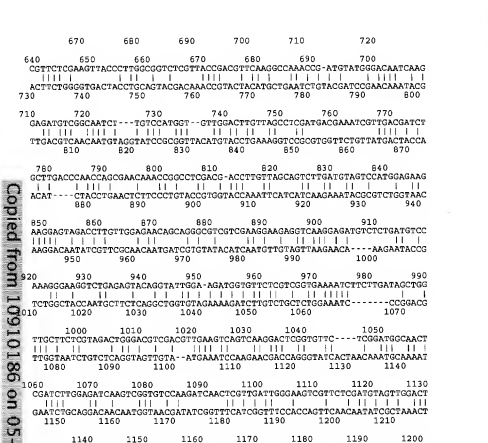
          290       300       310       320       330       340       350
          GAGTTGATGTCGTTGAAGTCGATGTTAATGTTGGACTTCTCCTTCTCGGAGTA---GATGTTGTATCTGTACT
          || | ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||  |  ||
          GAAATCATCTGG--ACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGA
          380       390       400       410       420       430       440

          360       370       380       390       400       410       420       430
          TGATGATCCTCCTCCAAAGCTTGGGCCTGTAGTTCAAGCCTTGTAC-ATACCCTCCTTGATGGTGTAGAAT
          || | ||  |  ||  |  ||  |  ||  |  ||  |  ||  | ||  |  ||  |  ||  |  ||
          TCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAA
          450       460       470       480       490       500       510

                    440       450       460       470       480       490
          TGGGTGTTGACGG-----TGGACAACATCATTGGGCGACGATCAACCGTACATGTCGGACCACTTCTCGTTTC
                | |  |||||   || ||||  |||  |  ||| |  |  ||  |  ||  |  ||  |  ||
          TCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACA
        520       530       540       550       560       570       580       590

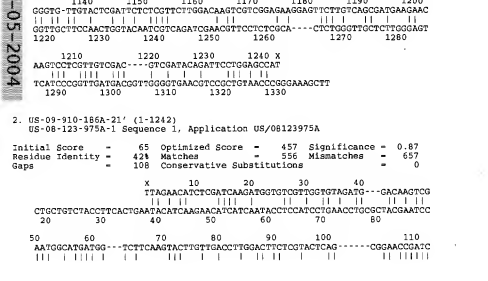
          500       510       520       530       540       550       560
          TCTTGGTCAAGCGTTGTCGATGGTCTTGATGATCTTGTTCTTGTTGTCGATGTAGGACTCCAA-CAAGAAG
          || || |||||  | | |  ||| |||  ||  |  ||| |  ||  ||  ||  ||  ||| ||| |  |
          TCATGTTCAAA--CTGGACGGTTGTCGTGACACTC-ACCGCTACATCTGGATCAAATACTTCAATCTGTTCG
                  600       610       620       630       640       650       660

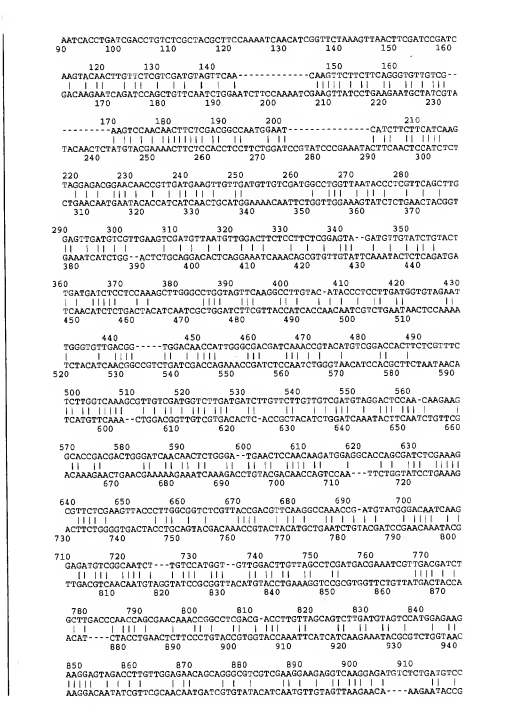
          570       580       590       600       610       620       630
          GCACCGACGACTGGGATCAACAACTCTGGGA--TGAACTCCAACAAGATGGAGGCACCAGCGATCTCGAAAG
            ||  ||  |  ||  ||  ||  ||  |  ||  ||||  ||  |  |  |  |  |  ||||  ||||
          ACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAA---TTCTGGTATCCTGAAAG
```



2. US-09-910-186A-21' (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	65	Optimized Score	=	457	Significance	= 0.87
Residue Identity	=	424	Matches	=	556	Mismatches	= 657
Gaps	=	108	Conservative Substitutions	=			= 0





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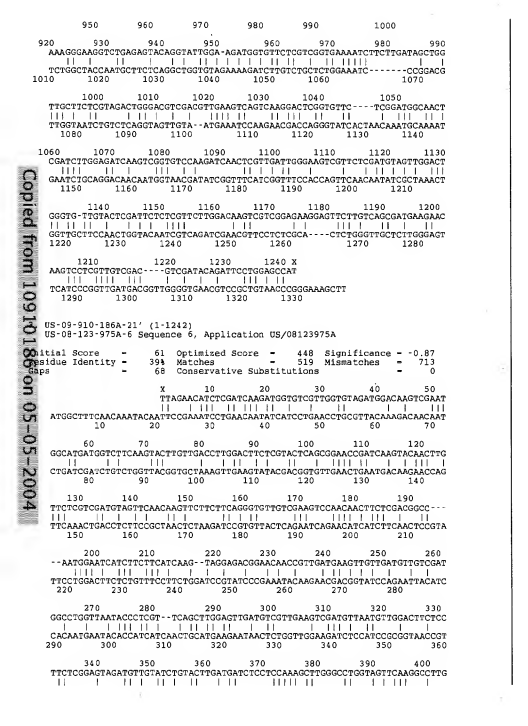
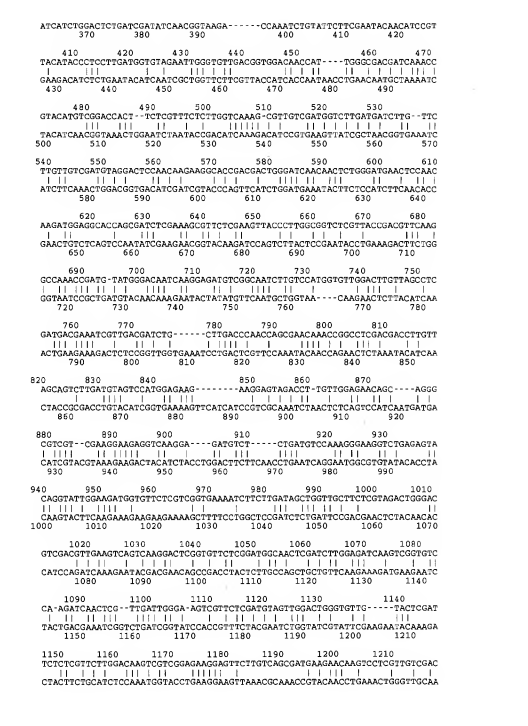
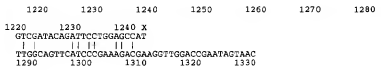
Copied from 10910186a on 05-05-2004



US-09-910-186A-21' (1-1242)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 61 Optimized Score = 448 Significance = -0.87
Residue Identity = 39% Matches = 519 Mismatches = 713
Gaps = 68 Conservative Substitutions = 0





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Copied from 10/910,186 on 05/14/2004

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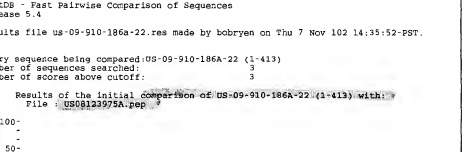
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-22.res made by bobryen on Thu 7 Nov 102 14:35:52-PST.


Query sequence being compared:US-09-910-186A-22 (1-413)
Number of sequences searched:                3
Number of scores above cutoff:               3

      Results of the initial comparison of US-09-910-186A-22 (1-413) with:
        File : US08123975A.pep
```



PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	20
Gap penalty	5.00	Window size	413
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	151	21	225.75

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	1704
Number of sequences searched:	3
Number of scores above cutoff:	3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	412	412	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	22	185	-0.57	0
3. US-08-123-975A-5	Sequence 5, Application U	439	20	184	-0.58	0

1. US-09-910-186A-22 (1-413)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score	=	412	Optimized Score	=	412
Residue Identity	=	100%	Matches	=	412
Gaps	=	0	Conservative Substitutions	=	0

Significance = 1.16
Mismatches = 0

```
X       10        20        30        40        50        60        70
MAPGICIDVDNEDLPFIADKNSPSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
APGICIDVDNELDFPIADKNSPSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
X       10        20        30        40        50        60        70

        80        90       100       110       120       130       140
DFNVDVPVYEKQPAIKKIPTDENTIPQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANKV
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DFNVDVPVYEKQPAIKKIPTDENTIPQYLYSQTFPLDIRDISLSSFDDALLFSNKVYSFFSMDYIKTANKV
        80        90       100       110       120       130       140

       150       160       170       180       190       200       210
VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALMVGNSTAKGNFENAFEIAGASILLEFIP
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALMVGNSTAKGNFENAPEIAGASILLEFIP
       150       160       170       180       190       200       210

       220       230       240       250       260       270       280
ELLIPVVGAPLLESYIDNKNKIIKTIDNALIKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNTQAQ
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ELLIPVVGAPLLESYIDNKNKIIKTIDNALIKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQ
       220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKLLDFDN
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKLLDFDN
290       300       310       320       330       340       350

       370       380       390       400       410  X
TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFP
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNWIILNLRYKD
360       370       380       390       400       410 X     420       430

N
```

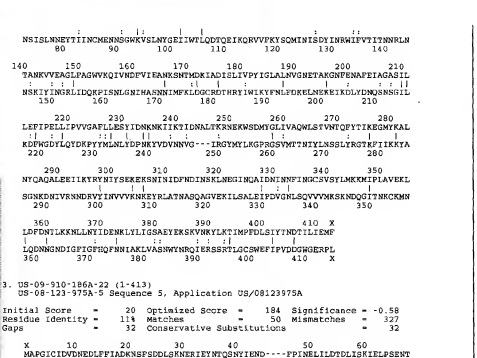
2. US-09-910-186A-22 (1-413)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score	=	22	Optimized Score	=	185
Residue Identity	=	8%	Matches	=	37
Gaps	=	3	Conservative Substitutions	=	31

Significance = -0.57
Mismatches = 342

```
        X       10        20        30        40        50        60
          MAPGICIDVDNEDLPFIADKNSPSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSEN
                                                  |  |  |  |  |  |  |  |  |
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKMAIVYNSMYENFSTSFWIRIPKYF
          X  10        20        30        40        50        60        70

 70        80        90       100       110       120       130
TESLTDFNVDVPVYEKQPAIKKIPTDENTIPQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIK
```



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3. US-09-910-186A-22 (1-413)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 20 Optimized Score = 184 Significance = -0.58
Residue Identity = 11% Matches = 50 Mismatches = 327
Gaps = 32 Conservative Substitutions = 32

Created from 10910186A.000 on 0

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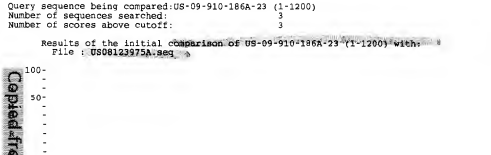
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

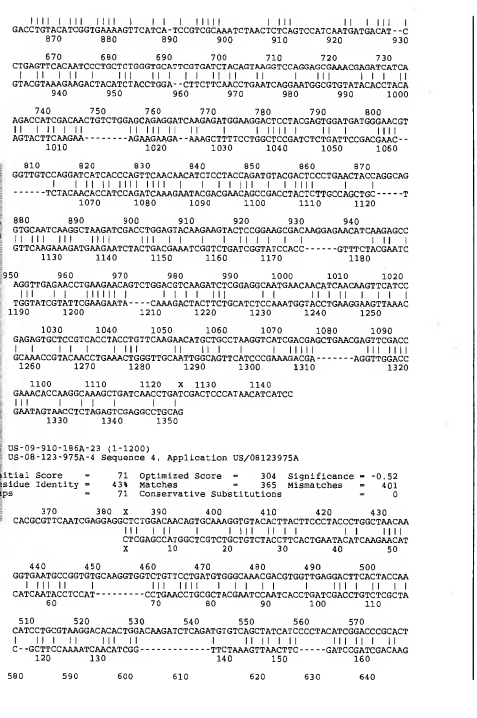
Results file us-09-910-186a-23.res made by bobryen on Thu 7 Nov 102 14:47:57-PST.

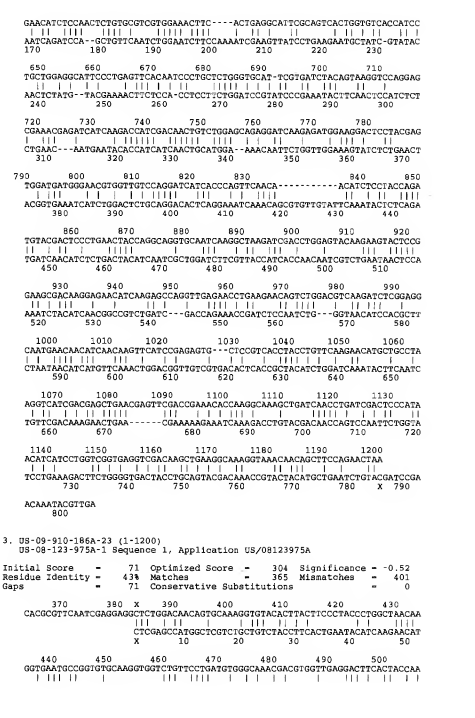

Query sequence being compared:US-09-910-186A-23 (1-1200)
Number of sequences searched:                3
Number of scores above cutoff:               3

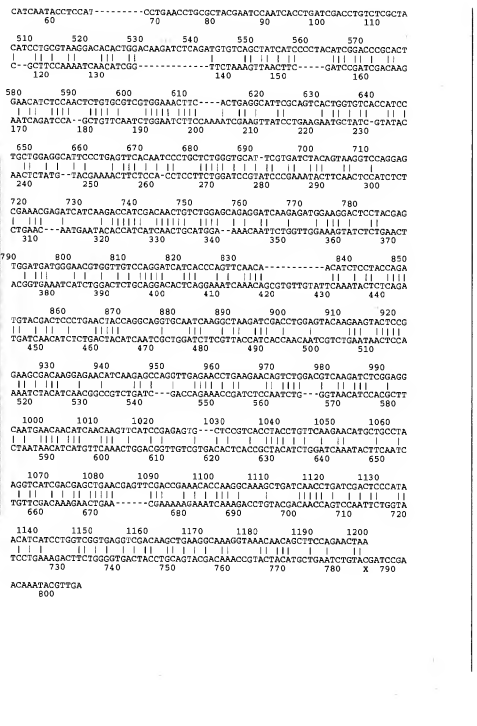
        Results of the initial comparison of US-09-910-186A-23 (1-1200) with:
          File : US08123975A.seq
```


100
50
10
5
0
|| | | |

Copied from 10910186 on 05-01-2004







Copied from 10910186 on 05-05-2004

Copied from 10916486 on 05/13/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23-inv.res made by bobryen on Thu 7 Nov 102 14:48:11-PST.


Query sequence being compared:US-09-910-186A-23' (1-1200)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-23' (1-1200) with:
          File : US08123975A.seq
```

Complement

```
                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                    SEARCH STATISTICS

Scores:                 Mean        Median     Standard Deviation
                          58            29                  25.98

Times:                   CPU                    Total Elapsed
                  00:00:00.00                 00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	73	449	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	73	449	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	28	440	-1.15	0

```
1. US-09-910-186A-23' (1-1200)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     73  Optimized Score  =    449  Significance =  0.58
Residue Identity  =    42%  Matches          =    527  Mismatches   =   653
Gaps              =     62  Conservative Substitutions               =     0

                        X       10        20        30        40        50
                        TTAGTTCTGGAAGCTGTTGTTTACCTTTGCCTTCAGCTTGTCGACCTCACCG
                        || || |||| | | | |||||  | | | | | | | | | | | | | | |
    CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCC
     20        30        40        50        60        70        80

         60        70        80        90       100       110       120
    ACCAGGATGATGTTAIGGGAGTCGATCAGGTTGATCAGCTTTGCCTTGGTGTTTCGGTCGAACTCGTTCAGC
    |    |||| | | |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    AATCACCTGAT-CGACCTGTCTCGCT-ACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
   90        100       110       120       130       140       150

        130       140       150       160       170       180       190
    TCGTCGATGACCTTAGCGAGCATGT---TCTTGACAGGTAGGTGACGGAGCACTCTCCGATGAACTTGTTC
    ||| | | | |  ||||    | | ||| |||           || ||  | | | | | | |   |
    TCGACAAGAATCAGATCCAGCTIGTTCAATCTGGAATCTTCCAAAATCGAAGTIATC-CTGAAGAATGCTATC
  160       170       180       190       200       210       220       230

        200       210       220       230       240       250       260
    ATGTTGTTCATTGCCTCCGAGATCTTGACGTCCAGACTGTTCTTCAGGTTCTCAACCTGGCICTTGATGTTC
    |  | |   | |  | | ||| |||  | | | | | | | | | | | | | | | | | | | | |||
    GTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGIATCCCGAAATACTTCAACTCCATC
           240       250       260       270       280       290       300

        270       280       290       300       310       320       330
    TCCTTGTCGCTTCCGGAGTACTTCTTTGTACTCCAGGTCGATCTTAGCCTTGATTGCACCTGCCTGGTAGTTC
    || ||  |   | |  | | | | ||| || | | | | | | | | | | | | | | | | | | | |
    TCTCTGAACAATGAATACACCATCATCAACTGCATCGTACGAACAAC-AATTCTCGTTGGAAAACTATCTCCAATA
          310       320       330       340       350       360       370

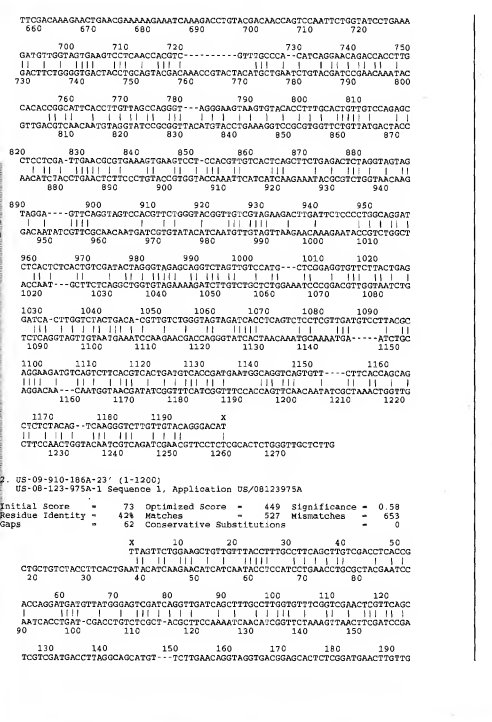
    340       350       360       370       380       390       400
    AGGGAGTCGTACATCTG------GTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGACAACCACGTTCCC
    ||  |  |||||| | | |||| | | | | | | | | | | | | | | | | | | | | | | | |
    CGG--TGAAATCATCTGGACTCTGCAGGACACTCAGGAATCAAACACGTGTTGTATTCAATACTCTCCAG
         380       390       400       410       420       430       440

        410       420       430       440       450       460       470
    ATCATCCACTCGTAGGAGTCCTTCCATCTCTTGATCCTCGTCCAGACAGTTGTCGATGGTCTTGATGATC
    || |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    ATGATCAACATCTCTGACTACATCAATCGCTGGACTTCTGTTACC--ATCACCAACAATCGTC-TGAATAAC
         450       460       470       480       490       500       510

     480       490       500       510       520       530       540
    TCGTTTCGCTCCTGGACCTTACTGTAGATCACGAATGCACCCAGAGCAGGGATTGTGAACTCAGGGAATGCC
    ||  |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    TCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCT
          520       530       540       550       560       570       580

    550       560       570       580       590       600       610
    TCCAGCAGGATGGTGACACCAGTGACTGCGAATGCCTCAGTGAACTTTCCACGACGCACAGAGTTGGAGATC
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    AATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTG
          590       600       610       620       630       640       650

  620       630       640       650       660       670       680       690
  TTCAGTGCGGGTCCGATGTAGGGGATGATAGCTGACACATCTGAGATCTTGTCC-AGTGTGTCCTACGCAG
  |||  |  | | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | |
```



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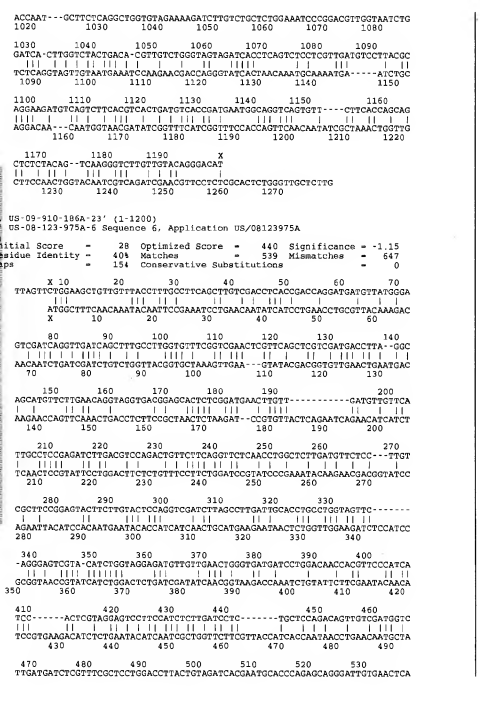
Copied from 10910186 on 05-05-2004



US-09-910-186A-23' (1-1200)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 28 Optimized Score = 440 Significance = -1.15
Residue Identity = 40% Matches = 539 Mismatches = 647
Gaps = 154 Conservative Substitutions = 0

Copied from 10910186a on 05/07/2004

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> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-24.res made by bobryen on Thu 7 Nov 102 14:36:15-PST.


Query sequence being compared:US-09-910-186A-24 (1-399)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-24 (1-399) with:
          File : US08123975A.pep
```

```
                                PARAMETERS

Similarity matrix       PAM-150     K-tuple                      1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty             20
Gap penalty                5.00     Window size                399
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                            SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                             74            19            96.71

Times:                      CPU                       Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                        1704
Number of sequences searched:                 3
Number of scores above cutoff:                3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	186	263	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	19	177	-0.57	0
3. US-08-123-975A-5	Sequence 5, Application U	439	18	175	-0.58	0

```
1. US-09-910-186A-24 (1-399)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   186  Optimized Score  =   263  Significance =  1.16
Residue Identity =   34% Matches          =   136  Mismatches   =   223
Gaps             =     1  Conservative Substitutions            =    33

           10        20        30        40        50        60        70
MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
          | | ||  |||||                 |         |         |         |
          APGICIDVDNEDLPFIADKNSFSDDLSKNERIEYNTQSWYIENDFPINELILDTDLISKIELPSE
          X        10        20        30        40        50        60

           80        90       100       110       120       130       140
YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVTYFFP-TLA
          :  :     :  :      :  |||||     :  :   |  :::|   | |||  :|    :
NTESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDILSLTSSFDDALLFSNKVVSFFSMDYI
    70        80        90       100       110       120       130

           150       160       170       180       190       200       210
NKVNAGVQGGLFLMWANDVVSDFTTNILRKDVTLDKISDVSAIIPYIGPALNISNSVRRGNFTEAFAVTGVTI
  |  ||||  |   :|||  |   ||     :  |:||||:|:|||||:|:  |   :|||  ||  : |  |
KIANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
140       150       160       170       180       190       200

           220       230       240       250       260       270       280
LLEAPPEFTIPALGAFVIYSKVQENNEIIKTIDNCLEQRIKRWKDSYEWWMGTWLSRIITQFNNISYQMYDS
|||  |   ||  |||  |  :  :|||||||  |  |  |  |  |  :  ||| : |||  |  |  :
LLEPIPELLIPVVGAFLLESYIDNKNIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
210       220       230       240       250       260       270       280

           290       300       310       320       330       340       350
LNYQAGAIKAIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVIDE
|||||  |  |  |  |  |||  :|||  |  |  |  |  |  |||  ||  |||||  |  |  |  :
LNYQAQALEEIIKYRYNIYSEKEKSSNIINDLSSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
          290       300       310       320       330       340       350

 360       370       380       390       X
LNEFDRNTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
| :||  |  |  |  |||  |||  :  :|||
LLDPDNFIKKNLLNYIDENKLYLIGSAEYEKSEVNKYLKTIMPFDLSIYTNDTLILEMFN
          360       370       380       390  X    400       410


2. US-09-910-186A-24 (1-399)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    19  Optimized Score  =   177  Significance = -0.57
Residue Identity =    7% Matches          =    30  Mismatches   =   342
Gaps             =     6  Conservative Substitutions            =    22

     X        10        20        30        40        50        60        70
MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
          |         |         :         |         :         |         ||
RYESNWHLIDLSRYASKINIGSKVNPDPIDKNQIQLFNLESSKISVILKNAIVYNSMTFNFSTSFWIRIPKY
X         10        20        30        40        50        60        70

         80        90       100       110       120       130       140
YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVTYFFPTLAN
: ||  |   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
FNSILSLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQM--NISDVINRWIEVTITNN
         80        90       100       110       120       130       140
```

Copied from 10910186 on 05-05-2004

```
   150       160       170       180       190       200       210
KVNAGVQGGLFLMWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPAL--NISNSVRRGNFTEAPAVTGVT
 :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
RLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNS
      150       160       170       180       190       200       210

   220       230       240       250       260       270       280
ILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWLSRIITQFNNISYQMYD
 :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
GILKDFWGDYLQYDKPYYMLNLYDPNKYV--DVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK
     220       230       240       250       260       270       280

 290       300       310       320       330       340       350
SLNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVID
 :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
YASGNKDNIVRNNDMVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDGQITNKCK
     290       300       310       320       330       340       350

360       370       380       390       X
ELNEFDRWTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
 :  :  :  :  :  :  :  :  :  :  :  :  :  :
MNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
  360       370       380       390       X 400       410


US-09-910-186A-24 (1-399)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     18  Optimized Score  =    175  Significance = -0.58
Residue Identity =    10%  Matches          =     45  Mismatches   =   325
Gaps             =      0  Conservative Substitutions             =    26

X         10        20        30        40        50        60        70
MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
  ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
FNKYNSEILNNILLNLRYKDWNLIDLSGYGAKVEVDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFL
X         10        20        30        40        50        60        70

      80        90       100       110       120       130       140
YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFPTLAN
  ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI----DINGKTKSVFFEYNIRE
      80        90       100       110       120       130       140

    150       160       170       180       190       200
KVNAGVQGGLFLMWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRGNFT----------
 :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DISEYINRWFPVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE
     150       160       170       180       190       200       210

    210       220       230       240       250       260       270
-------EAFAVTGVTILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWL
       :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
LSQSNIEEKYKIQSYEELKDFWGNPLMYNKEYYMFNWAGNKNSTIKLKKDSPVGEILTRSKYNQNSKYINYR
     220       230       240       250       260       270       280

          280       290       300       310       320       330
S-----RIITQFNNISYQMYDSLMYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNIN
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEKLFLAPISDSDEFYNTIQ
  290       300       310       320       330       340       350

340       350       360       370       380       390       X
KFIRECSVTYLFKNMLPKVIDELNEFDRNTKAKLIN---LIDSHNIILVGEVDKLKAKVNNSFQN
 :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
IKEYDEQPIYSCQLLFKKDESETDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQ
360       370       380       390       400       410       420 X

 FIPKDEGWTE
430
```

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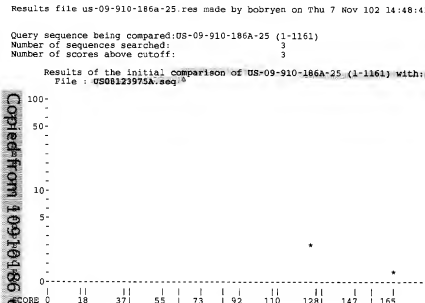
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25.res made by bobryen on Thu 7 Nov 102 14:48:41-PST.

Query sequence being compared:US-09-910-186A-25 (1-1161)
Number of sequences searched: 3
Number of scores above cutoff: 3

Result of the initial comparison of US-09-910-186A-25 (1-1161) with:
File : US08123975A.seq



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:

Mean	Median	Standard Deviation
139	127	22.52

Times:

CPU	Total Elapsed
00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	165	453	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	126	443	-0.58	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	126	443	-0.58	0

1. US-09-910-186A-25 (1-1161)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score	=	165	Optimized Score	= 453	Significance = 1.15
Residue Identity	=	43%	Matches	= 528	Mismatches = 610
Gaps	=	98	Conservative Substitutions	= 0	

```
X       10        20        30        40        50        60        70
ATGGCCAACTCCCGTGAGGACTCCACCTCGCATCAAGGTCAAGAACAACAGACTGCCATACGTTGCGCAGCAA-
|||||    |    |||  |    |||  |  |  |  |  ||||  |||  |  | ||||
ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAAT
X       10        20        30        40        50        60        70

        80        90       100       110       120       130
GGACTCCATCTCCCAGG---AGATCTTCGAGAACAAGATCATCACCGACGAGACC--AACGTTCAAAACTAC
  ||  ||||  |||  |   |  ||  ||||  |  ||  |  |||  |  ||   ||  |||  |||
CTGATCGATCCTGTCTGTTACGGTGCTAAAGTTGAAGTTATACGACGGTGTTGAACTGAATGACAAGAACCAG
        80        90       100       110       120       130       140

140       150       160       170       180       190       200
TCCGACAAGTTCTCTTTGGACGAGTC---CATCCTGGACGGTCAGGTCCCAATCAACCCAGAGATCGTCGAC
|||  |  ||||||  |  |  ||||     ||||  |  ||||  |  |  |||  |  |  ||  ||
TTCAAACTGACCTCCTCCGCTAACTCTAAAGATCCGTTTACTCAGAATCAGAACATCATCTTCAACTCCGTA
     150       160       170       180       190       200       210

210       220       230       240       250       260       270
CCACTGTTGCCAAACGTCAACATGAGCCATTGAACTTGCCAGGTGAGGAGATCGTCTTCTACGACGACATC
|||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TTCCTGGACTTCTCTGTTTCCTTGGATCCGTATCCCGAAATCAAGAACAGGTATCCAGAATTACATC
 220       230       240       250       260       270       280

280       290       300       310       320       330       340       350
ACCAAGTACGTCGACTACTTGAACTCCTACTACTACTTGCAGTCTCAAAAGTTGTCTAACAACGTCGAGAAC
|||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CACAATGAATACACCATCTCAACTGCATGAAGAAATAACTCTGGTTGAGAAGAACCCATCCGCGGTAACGGT
290       300       310       320       330       340       350       360

      360       370       380       390       400       410       420
ATCACCTTGACCACCTCCGTCGAGGAGGCCTTGGGTTACTCTAACAAGATC---TACACCTTCCTGCCATCC
|||||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTCGAATACAACATCCGTGAGAC
      370       380       390       400       410       420       430

      430       440       450       460       470       480       490
TTGGCTGAGAAGGTAACAAGGGTGTTCAAGCTGGTTGTTCCTGAACTGGGCCAACGAGGTCGTCGAGGAC
  |  ||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
ATCTCTGAATACATCAA----------TCGCTGG-TTCTTCGTTACCATCACCAATAACCTGAACAATG--
      440       450       460       470       480       490

      500       510       520       530       540       550       560
TTCACCACCAACATCATGAAGAAGGACACCCTGGACAAGATCTCCGACGTCTCCGTCATCATCCCATACATC
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
-------CTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATC
              500       510       520       530       540       550

  570       580       590       600       610       620       630
GGTCCAGCCTTGAACATC-GGTAACTCCGCCCCTGAGAGGTAACTTCAACGAGGCCTCCGCCACCGCCGGTGT
|  |  |  ||||  ||||  |  |||  |  |  |  ||||  |  |  |  |  |  |  |  |  |  |
GCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGT-ACCCAGTTCATCTGGATGAAATACTT
  560       570       580       590       600       610       620

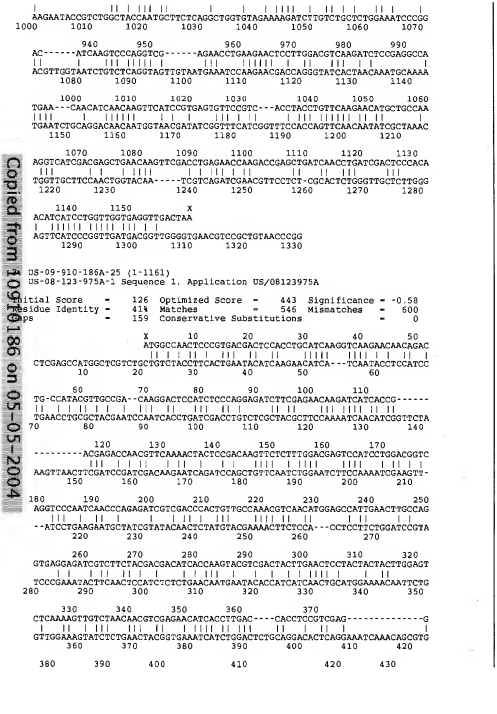
  640       650       660       670       680       690       700
CGCCTTCCTGCTGGAGGTTTTCCCAGAGTTCACCATCCCAGCCCTGGGTGTCTTCACCTTCTACTCCTCCAT
```

Copied from 10910186 on 05-05-2004

US-09-910-186A-25 (1-1161)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 126 Optimized Score = 443 Significance = -0.58
Residue Identity = 41% Matches = 546 Mismatches = 600
Gaps = 159 Conservative Substitutions = 0

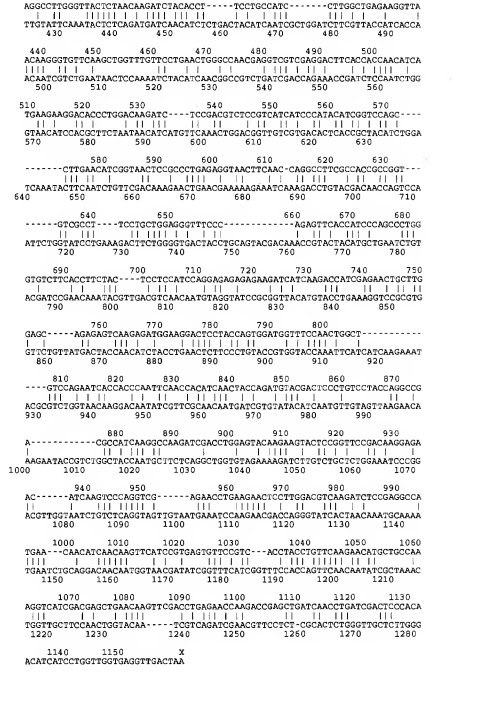
Copied from 10/910,186 on 05-05-2004

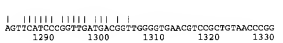


US-09-910-186A-25 (1-1161)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	126	Optimized Score =	443	Significance = -0.58
Residue Identity	=	41%	Matches =	546	Mismatches = 600
Gaps	=	159	Conservative Substitutions =		0

X 10 20 30 40 50
AGGGCCACTCCCGTGACGACTCCCACCTGCATCAAGGTCAACAACAGAC
CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCA---TCAATACCTCCATCC
10 20 30 40 50 60
60 70 80 90 100 110
TG-CCATACGTTGCCGA--CAAGGACTCCATCCTCCCAGGAGATCTTCGAGAACAAGATCATCACCG------
TGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTA
70 80 90 100 110 120 130 140
120 130 140 150 160 170
---------ACGAGACCAACGTTCCAAAACTACTCCGACAAGTTCTCTTTGGACGAGTCCATCCTGGACGGTC
AAGTTAACTGCTGATCCCGACAAGAACAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTT-
150 160 170 180 190 200 210
180 190 200 210 220 230 240 250
AGGTCCCAATCAACCCAGAGATCGTCGACCCACTGTTGCCAAAGTCAACATGGAGCCATTGAACTTGCCAG
--ATCCTGAAGATGCTATCGTATACAACCTCTATGTACGAAAAACTTCCCA---CCTCCTCCTGGATCCGTA
220 230 240 250 260 270
260 270 280 290 300 310 320
GTGAGGAGATCGTCTTCTACGACGACATCACCAAGTACGTCGACTACTTGAACTCCTACTACTACTTGGAGT
TCCCGAAATACTCTCAACTCCATCCTCTGAACAATGAATACACCATCACTCAACTGCATGGAAAACAATTCTG
280 290 300 310 320 330 340 350
330 340 350 360 370
CTCAAAAGTTGTCTAACAACGTCGAGAACATCACCTTGAC----CACCTCCGTCGAG----------G
GTTGGAAAGTATCCTCGAACTACGGTGAAATCATCTCGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
360 370 380 390 400 410 420
380 390 400 410 420 430





Copied from 10910186 on 05-05-2004

Copied from 10916486 on 05/20/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25-inv.res made by bobryen on Thu 7 Nov 102 14:48:57-PST.


Query sequence being compared:US-09-910-186A-25' (1-1161)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-25' (1-1161) with:
          File : 0808123975A.seq
```

```
                              PARAMETERS

Similarity matrix       Unitary      K-tuple                        4
Mismatch penalty              1      Joining penalty               30
Gap penalty                5.00      Window size                  500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                             41            33                    8.08

Times:                      CPU                       Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                                  Init. Opt.
Sequence Name      Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------------
  1. US-08-123-975A-4 Sequence 4, Application U  1338    46   205   0.62   0
  2. US-08-123-975A-1 Sequence 1, Application U  1338    46   205   0.62   0
                      **** 1 standard deviation below mean ****    -
  3. US-08-123-975A-6 Sequence 6, Application U  1351    32   246  -1.11   0


1. US-09-910-186A-25' (1-1161)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =    46  Optimized Score   =   205  Significance =  0.62
Residue Identity =   39%  Matches           =   236  Mismatches   =  336
Gaps             =    26  Conservative Substitutions =     0

  560       570       580       590       600       610       620       630
  ACCTCTCAGGGCGGGAGTTACCGATGTTCAAGAGCTGGACCGATGGATGGGATGACGACGAGCTCGGAGAT
                          |  |||| | | | |||  |   | | ||  |          |||
                          CTCGAGCCAGGCTCGTCTGCTGTCT---ACGTTCACTGAATACATCAAGAA
                        X        10        20        30        40

        640       650       660       670       680       690       700
  CTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTCGACGACCTCGTTGGCCCAGTTCAGGAA
  | |  ||    ||| | |  ||  | |  |  | |  |  ||||  | |  ||  | |  |  | |  |
  CATCATCAATACCTCCATCCTGAACCTG-----CGCTACGAATCCAAATCACCTGATCGACCTGTCTCGCTAC
50        60        70        80        90       100       110

        710       720       730       740       750       760       770
  CAAACCAGCTTGAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
  |  |  |  |||| |  | |||  | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  GCTTCAAAATCAACATCGGTTGTTCAAGTTAAC-TTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
  120       130       140       150       160       170       180

    780       790       800       810       820       830
  ACCCAAGGCCTCCTCGACGGAGGTGGTCAAGGTG-ATGTTCTCG--------ACGTTGTTAGACAACTTTTG
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGGCAAGTTATACAACTCTATGTACAAAACTTCTC
190       200       210       220       230       240       250

  840       850       860       870       880       890       900
  AGACTCCAAGTAGTAGTAGGAGTTCAAGTAGTCGACGTACTTGGTGATGTCGTCGTAGAAGACGATCTCCTC
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATCACACCATCATC
260       270       280       290       300       310       320

  910       920       930       940       950       960       970       980
  ACCTGGCAAGTTCAATGGCTCCATGTTGACGTTTGGCAACAGTGGGTCGACGATCTCTGGGTTGATTGGGAC
  | |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  AACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGAC
330       340       350       360       370       380       390       400

            990      1000      1010      1020      1030      1040
  ---CTGACCGTCCAGGATGGACTCG--TCCAAAGAGAACTTGTCGGAGTAGTTTGAACGTTGGTCTCGTCG
     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  ACTCAGGAAATCAAACAGCGTTGTATTCAAATACTCTCAGATGATCAACACTCTCGACTACATCAATCGAC
          410       420       430       440       450       460       470

1050      1060      1070      1080      1090      1100      1110      1120
  GTGATGATCTTGTTCTCGAAGATCTCCTGGGAGATGGAGTCCTTGTCGGCAACGTATGGCAGTCTGTTGTC
  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGAC
     480       490       500       510       520       530       540

          1130      1140      1150      X
  TTGACCTTGAT-GCAGGTGGAGTCGTCACGGGAGTTGGCCAT
  |  |||  |  |  |  |  |  |  |  |  |  |  |
  CAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGA
    550       560       570       580       590       600


2. US-09-910-186A-25' (1-1161)
   US-08-123-975A-1 Sequence 1, Application US/08123975A
```

Copied from 10910186 on 05-05-2004

```
Initial Score    =    46  Optimized Score  =   206  Significance =  0.62
Residue Identity =   39%  Matches          =   236  Mismatches   =   336
Gaps             =    26  Conservative Substitutions =             =     0

560       570       580       590       600       610       620       630
ACCTCTCAGGGCGGAGTTACCGATGTTCAAGGCTGACCGATGTATGGGATGATGACGGGAGACGTCGGAGAT
                                  |||||||||||||||||||||||||||||||||||||||
                                  CTCGAGCCATGGCTCGTCTGCTGTCT---ACCTTCACTGAATACATCAAGAA
                                  X        10        20        30        40

        640       650       660       670       680       690       700
CTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTCGACGACCTCGTTGGCCCAGTTCAGGAA
|| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CATCATCAATACCTCCATCGAACCTG-----CGCTACGAATCAATCACCTGATCGACCTGGTCCGCTAC
50        60        70        80        90       100       110

    710       720       730       740       750       760       770
CAAACCAGCTTAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCTTCCAAAATCAACATCGGTTCTAAAGTTAAC-TTCGATCCGATCGACAAGAATACGATCCAGCTGTTCAA
120       130       140       150       160       170       180

    780       790       800       810       820       830       840
ACCCAAGGCCTCCTCGACGGAGGTGGTCAAGGTG-ATGTTCTCG--------ACGTTGTTAGACAACTTTTG
|  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
190       200       210       220       230       240       250

840       850       860       870       880       890       900
AGACTCCAAGTAGTAGTAGGAGTTCAAGTAGTCGAGGTACTTGGTGATGTCGTCGTAGAAGACGATCTCCTC
|||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
260       270       280       290       300       310       320

910       920       930       940       950       960       970       980
ACCTGGCAAGTTCAATCGGCTCCATGTTGACGTTTGGCAACAGTGGGTCGACGATCTCTGGGTTGATTGGGAC
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACTGCATGGAAAACAATTCGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGAC
330       340       350       360       370       380       390       400

              990      1000      1010      1020      1030      1040
   ---CTGACCGTCCAGGATGGACTCG--TCCAAAGAGAACTTGTCGAGTAGTTTGAACGTTGGTCCTGTCG
      || |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
ACTCAGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGC
          410       420       430       440       450       460       470

1050      1060      1070      1080      1090      1100      1110      1120
GTGATGATCTTGTTCTCGAAGATCTCGTGGGAGATGGAGTCCTTGTCGGCAACGTATGGCAGCTCGTTGTTC
||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGAC
    480       490       500       510       520       530       540

          1130      1140      1150      X
TTGACCTTGAT-GAGAGTGGAGTCGTCACGGGAGTTGGCCAT
  ||  |||  | |  |  ||||||||||||||||||||||
CAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGA
  550       560       570       580       590       600

3. US-09-910-186A-25' (1-1161)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    32  Optimized Score  =   246  Significance = -1.11
Residue Identity =   40%  Matches          =   292  Mismatches   =   384
Gaps             =    51  Conservative Substitutions =             =     0

                  X        10        20        30        40        50
                  TTAGTCAACTCTCACCAACCAGGATGATGTTGTGGGAGTCGATCAGGTTGATC
                  |||||  |  |  |  ||  |  |  |  |||||||||||||||||||||||
ATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTG
      640       650       660       670       680       690       700
```

```
          60        70        80        90       100       110
AGCTCGGTCTTGGTT------CTCAGGTCGAACTTGTTCAGCTCGTCGATGACCTTTGGCAGCATGTTCTTG
|   |||  |  |  |     ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAACACTCT
       710       720       730       740       750       760       770

120       130       140       150       160       170       180
AACAGGTAGGTGACGGAACACTCACGGAT---GAACTTGTTGATGTTTGTTCATGGCCTCGGAGACTTGACG
|| |  |  |||  |  |||||||||||   ||||||||||||||||||||||||||||||||||||||||||
TACATCAAACTGAAGAAAGACTTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAA
  780       790       800       810       820       830       840

190       200       210       220       230       240       250
TCCAAGGAGTTCTTCAGGTTCTCGACCTGGGACTTGATGTTCTCCTTGTCGGAACCGGAGTACTTCTTGTAC
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TACATCAACTACCGCGACCTGTACATGGGTGAAAAGTTCATCATC-CGTCGCAAATCTAACTCTCAGTCCA-
  850       860       870       880       890       900       910

260       270       280       290       300       310       320
TCCAGGTCGATCTTGGCCTTGATGGCGTCGGCCTGGTAGGACAGGGAGTCGTACATCTGGTA-----GTTGA
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     |||||
TCAATGATGACATCGTACGTAAAGAAGACTACAT----CTACCTGGACTTCTTCAACCTGAATCAGGAATGC
  920       930       940       950       960       970       980

330       340       350       360       370       380       390
TGTGGTTGAATTGGGTGGTGATTCTGGACAGCCAGTTGGAAACCATCCACTGG--------TAGGAGTCCTT
|||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGTGTATACACCTACAAGTACTTCAAGAAAG-AAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGA
  990      1000      1010      1020      1030      1040      1050

          400       410       420       430       440       450       460
CCATCTCTTGACTCTCTGCTCCAAGCAGTTCTCGATGGTCTTGATGACTCTCTCTCTCCTCCTGGAGGAGGA
| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAA
 1050      1070      1080      1090      1100      1110      1120

     470       480       490       500       510       520       530
GTAGAAGCTGAAGACACCCAGGGCTGGGATGGTGAACTCTGGGAAACCTCCCAGCAGGAAGGCGACCGGC
|   |||||||   |  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||
G--AAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTCTACGAATCTGGTATCGTA
 1130      1140      1150      1160      1170      1180      1190

     540       550       560       570       580       590       600
GGTGGCGAAGGCCTGGTTGAAGT---TACCTCTCAGGGCGAGTTACCGATGTTCAAGGCTGACCGATGTA
|   |  |  |  |  |||||||   |||||||||||||||||||||||||||||||||||||||||||||||
TTCGAAGAATACAAAGACTACTTCTGCATTCTCAAATGGTACCTGAAGGAAGTTAAACGC-AAACGGTACAA
1200      1210      1220      1230      1240      1250      1260

     610       620       630       640       650       660       670
TGGGATGATGACGGAGACGTCGGAGATCTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTC
|   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CCTGAAACTGGGTTGCAATTGGCAGTCATCCCGA-------------AAGACGAAGGT--TGGACCGAAT
1270      1280      1290      1300                1310      1320

     680       690       700 X     710       720
GACGACCTCGTTGGCCCAGTTCAGGAACAAACCAGCTTGAACACCCT
     |||||  |  |  |  |  |  |  |  |  |  |  |  |
AGTAACCTCTACAGCTCGAGGCCTGCAG
  1330      1340      1350
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-26.res made by bobryen on Thu 7 Nov 102 14:36:40-PST.


Query sequence being compared:US-09-910-186A-26 (1-386)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-26 (1-386) with:
        File : US08123975A.pep

 100-
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```
130           140       150       160       170       180       190
  YSN-----KIYTFLPSLAREVNKGVQAGLFLNWANEVVEDFTTNIMKKDTLDKISDVSVIIPYIGPALNIGN
    :     :   :     :   :     :   :     :   :     :   :     :   :     :
  NSKIYINGRLIDQKPISNLGNIIASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
     150       160       170       180       190       200       210

  200       210       220       230       240       250       260
  SALRGNFNQAFATAGVAFLLEGFPEFTIPALGVFTFYSSIQEREKIIKT---IENCLEQRVKRWKDSYQWMV
    | :   |   :   |   :   |   :   |   :   |   :   |   :   |   :   |
  KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGN
   220       230       240       250       260       270       280

   270       280       290       300       310       320       330
  SNWLSRITTQFMHIWQMYDSLSYQADAIKAKIDLEYKKYSGSDKENIKSQVE-NLKNSLDVKISEAMNNIN
    |   :   |   :   |   :   |   :   |   :   |   :   |   :   |   :   |
  KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQD
 290       300       310       320       330       340       350       360

   340       350       360       370       380       X
  KFIRECSVTYLFKNMLPKVIDELNKFDLRTKTELINLIDSHNILVGEVD
    :   :   :   :   :   :   :   :   :   :   :   :
  NNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
         370       380       390       400       410


US-09-910-186A-26 (1-386)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     16  Optimized Score  =    101  Significance = -0.59
Residue Identity =     8%  Matches          =     21  Mismatches   =   204
Gaps             =      6  Conservative Substitutions               =    17

                       X       10        20        30                40
                       MANSRDDSTCIKVKNNRLPYVAKDDSIQEIFENKIITD------ETNVQNY
                       :   |   :   |   :   |   :   |   :   |   :   |
  SNTDIKDIREVIANGEIIPKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYN
          180       190 X     200       210       220       230       240

    50        60        70        80        90       100       110
  SDKFSLDESILDSQVPINPEIVDPLLPNVKMEPLNLPGEEIVFFDDITKYVDYLNSYYYLESQKLSNNVENI
    : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
  KEYYMPNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYI
     250       260       270       280       290       300       310

120       130       140       150       160       170       180       190
  TLTTSVEEALGYSNKIITFLPSLAEKVNKGVQAGLFLNWANEVVEDFTTNIMKKDTLDKISDVSVIIPYIGP
    |   :   |   :   |   :   |   :   |   :   |   :   |   :   |   :   |
  YLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDRESTDEIGLIG
    320       330       340       350       360       370       380

       200       210       220       230       240 X     250       260
  ALNIGNSALRGNFNQAFATAGVAFLLEGFPEFTIPALGVFTFYSSIQEREKIIKTIENCLEQRVKRWKDSYQ
       |:    :    :   :| |    :    :    :    :    :    :    :    :    :
  IHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQPIPKDEGWTE
  390       400       410       420       430       X
```

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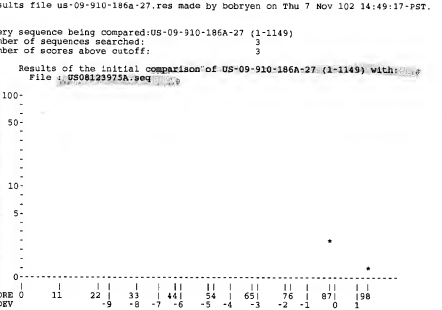
PastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27.res made by bobryen on Thu 7 Nov 102 14:49:17-PST.

Query sequence being compared:US-09-910-186A-27 (1-1149)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-27 (1-1149) with:
File : US08123975A.seq



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	90	87	6.93

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	98	463	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	86	408	-0.58	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	86	408	-0.58	0

1. US-09-910-186A-27 (1-1149)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score	=	98	Optimized Score	= 463	Significance = 1.15
Residue Identity	=	43%	Matches	= 561	Mismatches = 576
Gaps	=	144	Conservative Substitutions		= 0

```
                                X      10        20        30        40        50
                                ATGTCCATCTGCATCGAGATCAACAACGGTGAGCTGTTCTCGTGGCTTCCG
                                |  ||||  |  |  |  |||| |  |  |  |||  |  |  ||  | |
      ACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG
        20        30      X 40        50        60        70        80

            60        70        80        90       100       110
      AGAACAGTTACAACGATGCAACAACATCCTACTTAAGGAGATTGACGA---------CACCGTCACTTCTA
        || ||  ||  || |||       | ||  |  | || ||||  |         ||  | || |||
      GTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTT
      90        100       110       120       130       140       150       160

            120       130       140       150       160       170       180
      ACAACAACTACGAAAAGCACCTGGACCAG---GTCATCCTAAACTTCAACTCCG-AGTCCGCCCTGGTCTG
        |  ||||   | | |  |  |  |||     | |  | |||||||||| | |||     ||  |||| |
      CCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACACATCTTCAACTCCGTATTCGTGGACTTCTCTG
                170       180       190       200       210       220       230

                190       200       210       220       230       240       250
      --TCCGACGAGAAGCTGAACCTGACCATCCAGAACGACGCTTACATCCCAAAGTACGACTCCAACGGTACAT
        ||| |  | |  | | | ||  |  |||  |  |  |||  |  |  |||  |  |  |||  |  |  |
      TTTCCTTCTGGATCCGTACCCGAAATACAAGAACGACGGT---ATCCAGAATTACATCCAGA-TGAATAC
                240       250       260       270       280       290       300

            260       270       280       290       300       310       320
      CCGATATCGAGCAGCATGACG-TTAACGAGCTT---AACGTCTTCTTCTACTTAGACGCTCAGAAGGTGCCC
        |  | | |||||  | |||| |  |  |||   |  |  |  |  |  |  |  |  |  |  |  |
      ACCATCATCAACTGCATCAAGAATACTCTGGTTGGAGTCCATCCGGTAACGTATCATCTCGAGGACT
                310       320       330       340       350       360       370

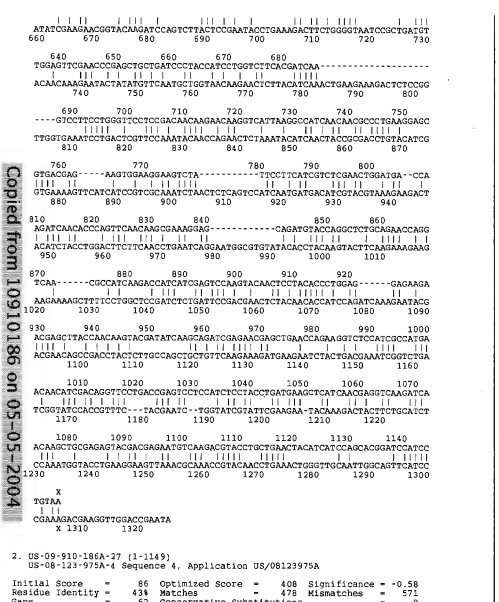
            330       340       350       360       370       380
      GAGGGTGAGAACAACG--------TCAATCTCACCTCTTCAATTGACACAGCCTTGTTGGAGCAGCCTA--AG
        |  |  |  ||||        |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      CTGATCGATATCAACGGTAAGACCAAATCGTATTCTTCGAATACAACGCCGTGAAGACATCTCTGAATAC
            380       390       400       410       420       430       440

            390       400       410       420       430       440       450
      ATCTACACCTTCTTCTCCTCCGAGTTCATCAACAACGTCAACAAGCCTGTGCAGGCCGCATTGTTCGTAAGC
      |||  |  ||||  |  |  |  |||  |||| |  |  |  |  |  |  |  |  |  |  |  |  |
      ATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGC--TAAAATCTACATCAACGGTAAAC
        450       460       470       480       490       500       510

      460       470       480       490       500       510       520
      TGGATTC--AGCAGGTGTTAGTAGACTTCACT---ACTGAGGCTAACCAGAAGTCCACTGTTGACAAGATCG
      |||| |  |  |  |  ||||  |  |  |   |||||  |  |  |  |  |  |  |  |  |  |  |
      TGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACG
        520       530       540       550       560       570       580

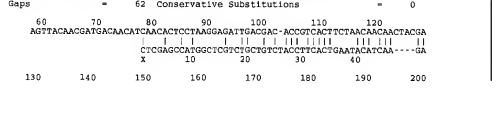
            530                                 540       550       560
      CTGACAGC----------------------------TCCATCGTCGTCCCATACATCGGTCTGGCTCTGAACA
            |||||||                       | | |  |  |  |  |||| |  |  |  |  ||
      GTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCA
        590       600       610       620       630       640       650

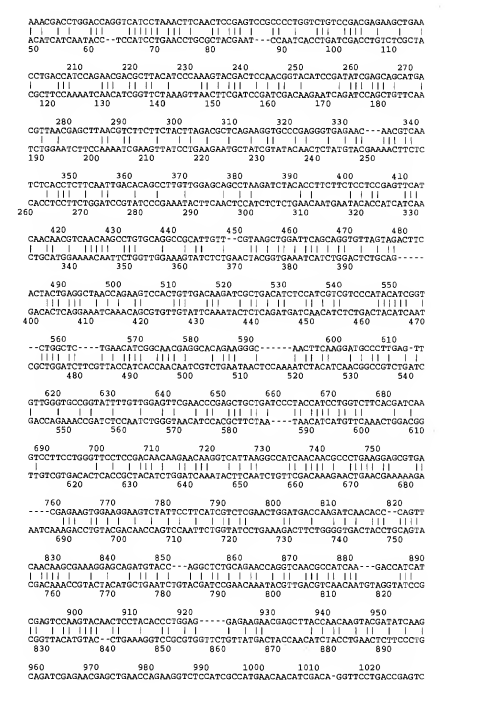
      570       580       590       600       610       620       630
      TCGGCAACGAGGCACAGAAGGGC------AACTTCAAGGATGCCCTTGAGTTGTTGGGTGCCGGTATTTTGT
```



2. US-09-910-186A-27 (1-1149)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 86 Optimized Score = 408 Significance = -0.58
Residue Identity = 43% Matches = 478 Mismatches = 571
Gaps = 62 Conservative Substitutions = 0





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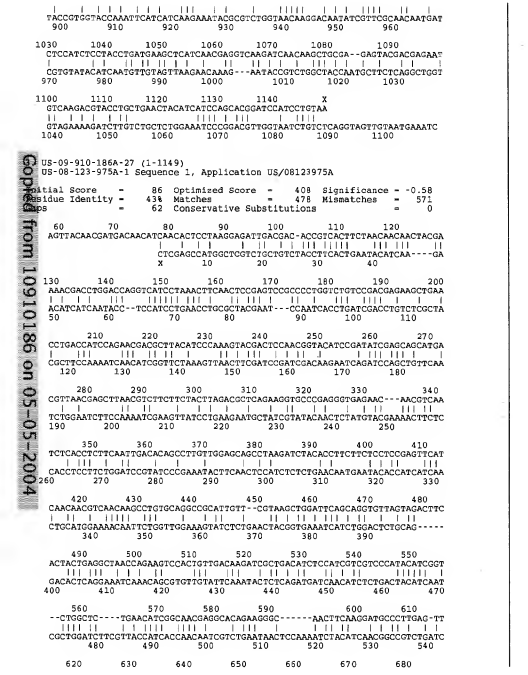

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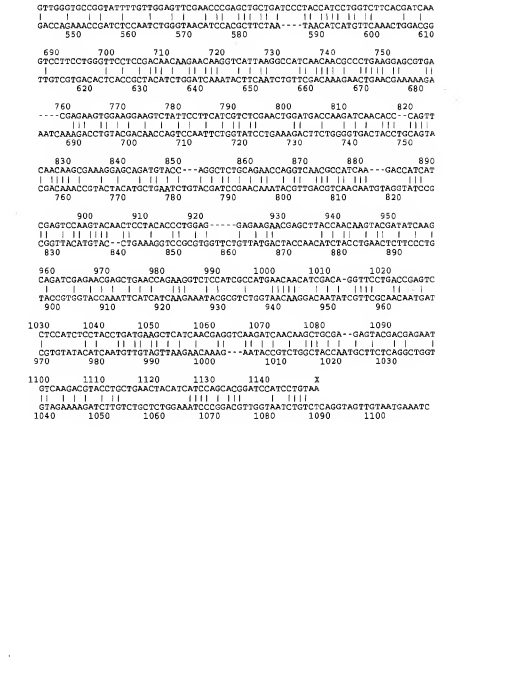
US-09-910-186A-27 (1-1149)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Optimal Score = 86 Optimised Score = 408 Significance = -0.58
Residue Identity = 43% Matches = 478 Mismatches = 571
Gaps = 62 Conservative Substitutions = 0



Copied from 10/910,186 on 05 Nov 2004

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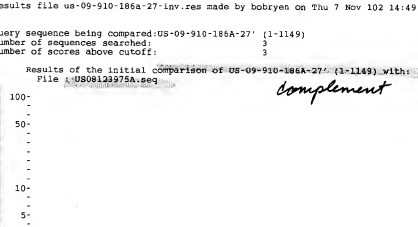
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27-inv.res made by bobryen on Thu 7 Nov 102 14:49:34-PST.

Query sequence being compared:US-09-910-186A-27' (1-1149)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-27' (1-1149) with:
          File : US08123975A.seq
```

complement




```
                              PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                  Mean        Median      Standard Deviation
                           38            38                    1.73

Times:                    CPU                    Total Elapsed
                  00:00:00.00                    00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6	Sequence 6, Application U	1351	40	359	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4	Sequence 4, Application U	1338	37	400	-0.58	0
3. US-08-123-975A-1	Sequence 1, Application U	1338	37	400	-0.58	0

```
1. US-09-910-186A-27' (1-1149)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    40 Optimized Score   =   359  Significance =  1.15
Residue Identity =   40% Matches          =   416  Mismatches   =   569
Gaps             =    54 Conservative Substitutions             =     0

  120        130        140        150        160        170        180        190
  GAGGACTCGGTCAGGAACCTGTCGATGTNGTTCATGGCGATGGAGACCTTCTGGTTCAGCTCCTTCTCATC
                                                                  | | | | | |
                                ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                              X         10         20         30         40         50

        200        210        220        230        240        250        260
  TGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTTCCTCCAGGGTTGTAGGAGTTGTACTTGGACTCGCATG
  ||| | |  |  |  | |||| |                 | ||||   ||||| | |          || ||
  TGCCTTA---CAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTG
            60         70         80         90        100        110        120

        270        280        290        300        310        320        330
  ATGGTCTTGATGGCGTTGACCTGGTCTGCAGAGCCTGGTACATCTGCTCCTTTCGCTTGTTGAACTGGGTG
   ||  ||  |||  |  |  |  |||  | |  |  |  |  |||  |  |  |  |  |  |  |  |  |
  TTGAACTGAACGACAAGACGAGTTCAAACTGA-CCTCTTCCGCTAAGCTCTAAGATCCGTGTTACTGAGAAT
            130        140        150        160        170        180        190

     340        350        360        370        380        390        400
  TTGATCTTGGTCATCCAGTTCGAGAGCGATGAAGGAATAGACTTCCTTCCACTTCTCGTCACGCTCCTTCAGG
   | | |  | ||  | |  | ||  |  |  |  |  |  |||||  |  |  |  |  |  |  |  |  |
  CAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAG
         200        210        220        230        240        250        260

  410        420        430        440        450        460        470
  GCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGAACCCAGGAAGGACTTGATCGTGAAGACC
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  --AACGACGGTATCCAGAATTACACCACAAT-------GAATACACCATCATCAACTGCATGAAGAATAAC
            270        280        290        300        310        320

  480        490        500        510        520        530        540
  AGGATGGTAGGGATCAGCAGCTCGGGTTCGAACTCCAACAAAATACCGGCACCCAACAAC-TCAAGGGCATC
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TCTGGTTGGAAGTCTCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAA
  330        340        350        360        370        380        390

  550        560        570        580        590        600        610        620
  CTTGAAGTTGCCCTTCTGTGCCTCGTTGCCGATGTTCAGAGCCAGACCGATGTATGGGACGAGGATGGAGAT
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  TCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCACGCTGGTTCTTCGTT---ACC
  400        410        420        430        440        450        460

        630        640        650        660        670        680        690
  GTCAGCGATCTTGTCAACAGTG--GACTTCTGGTTAGCCTCAGTAGTGAAGCTCACTAACACCTGCTGAATC
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  ATCACCAATAACCTGAACAATGCTAAAACTCACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGAC
  470        480        490        500        510        520        530        540

        700        710        720                   730        740        750
  CAGCTTACGAACAATGCGGCCTGCACAGGCTTGTT-------GACGTTGTTGATGAAC--TCGGAGGAGAAG
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  ATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATC
        550        560        570        580        590        600        610

     760        770        780        790        800        810        820
  AAGGTGTAGATCTTAGGCTGCTCCAACAAGG--CTGTGTCAATTGAAGAGGTGAGATTG--ACGTTGTTCTC
```

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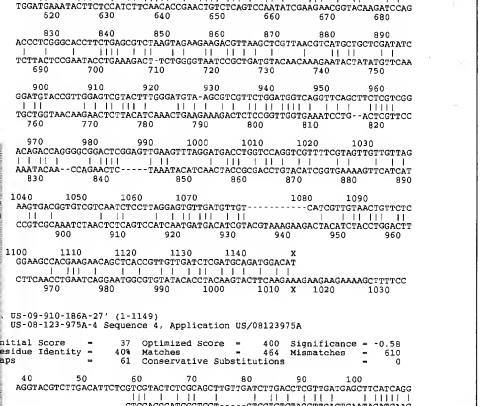
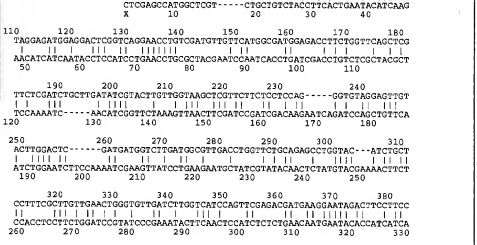
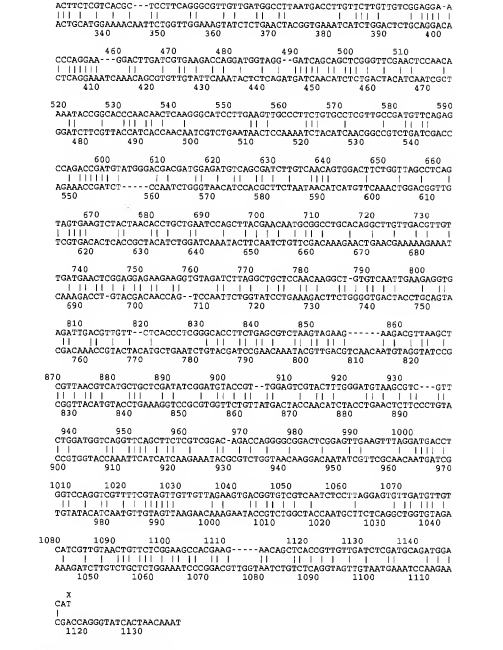


US-09-910-186A-27' (1-1149)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 37 Optimized Score = 400 Significance = -0.58
Residue Identity = 40% Matches = 464 Mismatches = 610
Gaps = 61 Conservative Substitutions = 0





3. US-09-910-186A-27' (1-1149)

Copied from 10910186 on 05-05-2004

```
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    37  Optimized Score  =   400  Significance = -0.58
Residue Identity =   40%  Matches         =   464  Mismatches   =   610
Gaps             =    61  Conservative Substitutions =     0

    40        50        60        70        80        90       100
AGGTACGTCTTGACATTCTCGTCGTACTCTCGCAGCTTGTTGATCTTGACCTCGTTGATGAGCTTCATCAGG
                                                                        
                                CTCGAGCCATGGCTCGT-----CTGCTGTCTACCTTCACTGAAGTCATCAAG
                               X         10        20        30        40

   110       120       130       140       150       160       170       180
 TAGGAGATGGAGGACTCGGTCAGGAACCTGTCGATGTTGTTCATGGCGATGGAGACCTTCTGGTTCAGCTCG
                                                                        
 AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCT
  50        60        70        80        90       100       110

      190       200       210       220       230       240
  TTCTCGATCTGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTTCTCCTCCAG-----GGTGTAGGAGTTGT
                                                                        
  TCCAAATC-----AACATCGGTCTCAAAGTTAACTTCGATCCGATCGACAAGATCAGATCCAGCTGTTCA
120       130       140       150       160       170       180

  250       260       270       280       290       300       310
  ACTTGGACTC------GATGATGGTCTTGATGGCGTTGACCTGGTTCTGCAGAGCCTGGTAC---ATCTGCT
                                                                        
  ATCTGGATCTTCCAAAATCGAAGTTATCCTGAAGAATGTATCGTATACAACTCTATGTACGAAACTTCT
   190       200       210       220       230       240       250

      320       330       340       350       360       370       380
  CCTTTCGCTTGTTGAACTGGGTGTTGATCTTGGTCATCCAGTTCGAGACGATGAAGGAATAGACTTCCTTCC
                                                                        
  CCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCCTGAACAATGAATACACCATCATCA
260       270       280       290       300       310       320       330

     390       400       410       420       430       440       450
  ACTTCTCGTCACGC---TCCTCAGGGCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGA-A
                                                                        
  ACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACA
       340       350       360       370       380       390       400

      460       470       480       490       500       510
  CCCAGGAA---GGACTTGATCGTGAAGACCAGGATGGTAGG--GATCAGCAGCTCGGGTTCGAACTCCAACA
                                                                        
  CTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCT
       410       420       430       440       450       460       470

520       530       540       550       560       570       580       590
  AAATACCGGCACCCAACAACTCAAGGCATCCTTGAAGTTGCCCTTCTGTGCCTCGTTGCCGATGTTCAGAG
                                                                        
  GGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACC
   480       490       500       510       520       530       540

      600       610       620       630       640       650       660
  CCAGACCGATGTATGGGACGACGATCGCAGCCATCTTGTCAACACTGGACTTCGGTTACGCTCAG
                                                                        
  AGAAACCGATCT-----CCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTG
   550       560       570       580       590       600       610

     670       680       690       700       710       720       730
  TAGTGAAGTCTACTAACACCTGCTCGAATCCAGCTTACGACAATGCGGCCTGCACAGCTTGTTGACGTTGT
                                                                        
  TCGTGACACTCACGGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAAT
   620       630       640       650       660       670       680

   740       750       760       770       780       790       800
  TGATGAACTCGGAGGAGAAGAAGGTGTAGATCTTAGGCTGCTCCAACAAGGCT-GTGTCAATTGAAGAGGTG
                                                                        
  CAAAGACCT-GTACGACAACCAG---TCGAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
   690       700       710       720       730       740       750

  810       820       830       840       850       860
```

```
  AGATTGACGTTGTT--CTCACCCTCGGGCACCTCTCTGAACGTCTAAGTAGAAG------AAGACGTTAAGCT
                                                                        
  CGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCG
     760       770       780       790       800       810       820

870       880       890       900       910       920       930
  CGTTAACGTCATGCTGCTCGATATCGGATGTACCGT--TGGAGTCGTACTTTGGGATGTAAGCGTC---GTT
                                                                        
  CGGTTACATGTACCTGAAAGGTCGGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTA
   830       840       850       860       870       880       890

   940       950       960       970       980       990      1000
  CTGGATGGTCAGGTTCAGCTTCTCGTCGGAC-AGACCAGGGCGGACTCGGAGTTGAAGTTTAGGATGACCT
                                                                        
  CCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCG
900       910       920       930       940       950       960       970

1010      1020      1030      1040      1050      1060      1070
  GGTCCAGCTCGTTCGTAGTTGTTGTTAGAAGTGACGGTCGTCGTCAATCTCCTTAGGAGTGTTGATGTTGT
                                                                        
  TGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGA
          980       990      1000      1010      1020      1030      1040

1080      1090      1100      1110      1120      1130      1140
  CATCGTTGTAACTCCTCTCGGAAGCCACGAAG-----AACAGCTCACCGTTGTTGATCTCGATGCAGATGGA
                                                                        
  AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAA
     1050      1060      1070      1080      1090      1100      1110

   X
  CAT
  |
  CGACCAGGGTATCACTAACAAAT
    1120      1130
```

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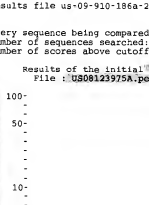
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-28.res made by bobryen on Thu 7 Nov 102 14:37:06-PST.


Query sequence being compared:US-09-910-186A-28 (1-382)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-28 (1-382) with:
          File : US08123975A.pep
```




```
                                PARAMETERS

Similarity matrix          PAM-150     K-tuple                      1
Threshold level of sim.        16%
Mismatch penalty                1     Joining penalty             20
Gap penalty                  5.00     Window size                382
Gap size penalty             0.05
Cutoff score                    1
Randomization group             0

                           SEARCH STATISTICS

Scores:                      Mean       Median      Standard Deviation
                               69           15                   93.83

Times:                        CPU                      Total Elapsed
                      00:00:00.00                      00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	178	270	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	17	175	-0.55	0
3. US-08-123-975A-5	Sequence 5, Application U	439	14	173	-0.59	0

```
1. US-09-910-186A-28 (1-382)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   178  Optimized Score  =   270  Significance =  1.16
Residue Identity =   41%  Matches          =   157  Mismatches   =   185
Gaps             =     7  Conservative Substitutions             =    33

       X          10         20         30         40         50         60         70
 MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNNYENDLDQVILNFNSESAPGLSDEKLNLTIQ
  |||:: | :|||:|  ||: ||  |  :  |  :  |  ||  |  |  |  |  |  |  |  |  |  |
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLTD
 X         10         20         30         40         50         60         70

        80         90        100        110        120        130        140
NDAYIFKTDSNGTSDIEQHDVNELNWVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTPFSSEFINNVNK
  :| |:    |  |  :| || :|  |  : |||| | |||  |:| |||  ::|  ||  |  |  |  ||
FNVDVPVFEKQPA--IKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANK
         80         90        100        110        120        130        140

       150        160        170        180        190        200        210
PVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVPYIGLALNVGNEAQKGNFKDALELLGAGILLEFE
 | |:||  |: |:  ||  |||  | |||||| :|||||||:|||  ||||  | |  || |||||
VVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFSNAFEIAGASILLEFI
        150        160        170        180        190        200        210

       220        230        240        250        260        270        280
PELLIPTILVFTIKSFLGSSDNKNKVIKAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKKKEQMYQALQ
|||||| :  |:  |  ||||:|:|  | |||  | ||| : |  |  ||: : :||||  || || ||
PELLIPVVGAFLLESYI--DNKNKIIKTIDNALTKSNEKWSDMTGLIVAQWLSTVNTQFTIKEGMYKALN
       220        230        240        250        260        270        280

       290        300        310        320        330        340        350
NQVNAIKTIISSKYNSYTLEEKNELTNKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINK
 |  |  |  ||| |  ||  |  |  |  |  |  |  :  |  ||  |  |  |:||||  : |
YQAQALEEIIKYRNIVSEKEKSNI--NDFNDINSKLNDSINQAIDNINNFINGCSVSYLMKKMIPLAVEK
       290        300        310        320        330        340        350

  360        370        380 X
LREYDENVKYLLNNYIIQHGSIL
| ::|  |  ||||
LLDFDFNTLKKHLLWIDENKLYLIGSAEYESKSVNKYLKTIMP
       360        370        X 380      390

2. US-09-910-186A-28 (1-382)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    17  Optimized Score  =   175  Significance = -0.55
Residue Identity =   10%  Matches          =    40  Mismatches   =   320
Gaps             =     6  Conservative Substitutions             =    22

         X          10         20         30         40         50         60
  MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNNYENDLDQVILNFNSESAPGLSDEKLN
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
RYESNNLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIYYNSMYENFSTSFWFNIRPKYF
       X  10         20         30         40         50         60         70

  70         80         90        100        110        120        130
LTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSSEFIN
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
NSISLNNETTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINSWIFVTITNNRLN
         80         90        100        110        120        130        140
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29.res made by bobryen on Thu 7 Nov 102 14:49:57-PST.


Query sequence being compared:US-09-910-186A-29 (1-1227)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-29 (1-1227) with:
          File : US08123975A.seq

 100-
    |
    |
  50-
    -
    -
    -
    -
    -
  10-
    -
    -
   5-
    -
    -
    -
    -
    -
   0-----------------------------------------------------------------------
    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
SCORE 0    6    12   18   24   29   |  351  |  41  |  47   |  53
STDEV                    -9  -8  -7  -6  -5  -4  -3  -2   -1   0


                              PARAMETERS

Similarity matrix       Unitary     K-tuple                      4
Mismatch penalty              1     Joining penalty             30
Gap penalty                5.00     Window size                500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             51           49                   2.89

Times:                      CPU                     Total Elapsed
                    00:00:00.00                     00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	53 412	0.69	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	53 412	0.69	0
	**** 1 standard deviation below mean ****				
3. US-08-123-975A-6	Sequence 6, Application U	1351	48 412	-1.04	0

```
1. US-09-910-186A-29 (1-1227)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    53  Optimized Score   =    412  Significance =  0.69
Residue Identity  =   439  Matches          =    439  Mismatches   =   633
Gaps              =    64  Conservative Substitutions =              =     0

          50        60  X    70        80        90       100       110
TTATTCTTTGTCGCCTCCGAGTCAAGCTACAACGAGAACGATAT-TAACACACCTAAAGAGATTGACGATAC
                          ||||| | | | | | | | | | | | | | | | | | | | | | |
                        CTCGAGCCATGGCTGCTCGTCTGCTCTACCTTCACTGAATACATCAAGAACAT
                        X         10        20        30        40        50

     120       130       140       150       160       170       180
TACCAACCTAAACAACAACTACCGGAACAACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCC
| |||  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CATCAATACCTCCATCCTGAACCTGCGCTAC---GAATCCAATCACCTGATCGACCGTGTCTGGCTAGCGTTC
        60        70        80        90       100       110       120

     190       200       210       220       230       240       250
TCAAATTTCCAACCGTACCTTAAACACTCTTGTCCAAGACAAC--TCCTACGTTCCAAGATACGATTCTAAC
| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCT--G
        130       140       150       160       170       180       190

     260       270       280       290       300       310       320
GGTACCTCAGAGATCGAGGAGTATGATGTTGTTGACT-TTAACGTCTTTTTCTATTTGCATGCCCAGAAGGT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
GAATCTTCCAAAATCGAAG----TTATCCTGAAGAATGCTATCGTATACAACTCTATG--TACGAAAACTTC
        200       210       220       230       240       250

     330       340       350       360       370       380       390
GCCAGAAGGTGAAACCAACATCCATTGACTTCTTCCATTGATACCGCCTTGTTGCAAGAGTCCAGGGATAT
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
TCCACCTCCTCTGGATCCGTATCCCGAAATACTTCAACT----CCATCTCTCTGAACAATGAATACACCAT
260       270       280       290       300       310       320

400       410       420       430       440       450       460       470
CTTCCTTTCTCCGGAGTTTATCGATACTATCAACAAGCCTGTCAACGCCGCTGCTCATTGATTGGATTAG
|||  |  |||  |  |  |  |  ||  |  || |  |||  |  |  |  ||||  |  |  |  |
CATCAACTGCATGGAAACAATTCCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCAT--CTGGACTCTG
 330       340       350       360       370       380       390

          480       490       500       510       520       530       540
CAAGGTCACTA-GAGATTTACCACTGAAGCTACTCAAAAGTCCACTGTTGAT-AAGATTGCTCACATCTCT
|| |   ||| ||  |||   ||  |   ||  |||||   | |  |||| || ||  |||||
CAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGAC------
  400       410       420       430       440       450       460

     550       560       570       580       590       600       610
TTGATTGTCCCCTATGTGGGTCTTGCTTTGAACATCATT--ATTGAGGCAGAAAAGGGTAACTTTGAGGAGG
|  ||  |  ||  |  ||  |  | |||  |  |||  |  |  |  |  |  |  |  |  |  |  |
TACATCAATCGCTGGATCCTGGTTACATCACCAACAAACGTCTCGAATAACTCCAAAATCTACATCAAGGGC
     470       480       490       500       510       520       530

     620       630       640       650       660       670       680
CTTTTGAATTGTTGGGAGTTGGTATTTTGTTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTT
| | |||   | |  | |  |  |  |  |||||  |||  |||  |  |  |  |  |  |  |  |
CGTCTGATCGACCAGAAACGGATCTCCAATCTGGCTAACATCCA-CGCTTCTAATAACATCATGTTCAAACT
     540       550       560       570       580       590       600

          690       700       710       720       730       740       750
TTACG---ATCAAGTCCTACATCGATTCATACGAGAACAAGAATAAAGCAATTAAAGCTATTAACAACTTCCT
   |||    ||  | |  || ||  | |||  |  || ||  ||||  ||||      | |  || ||||
```

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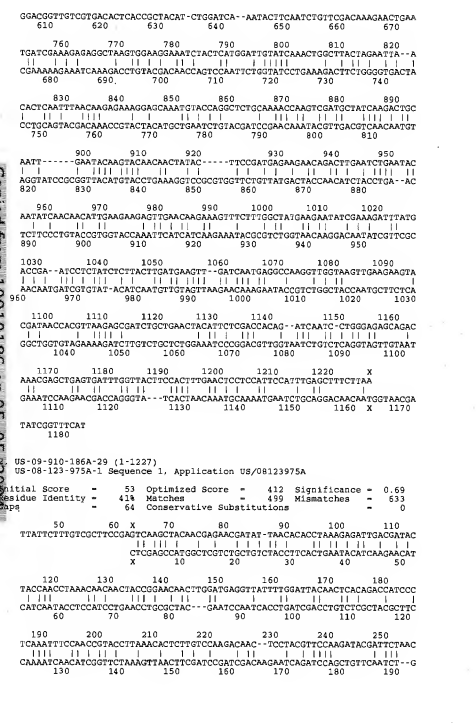
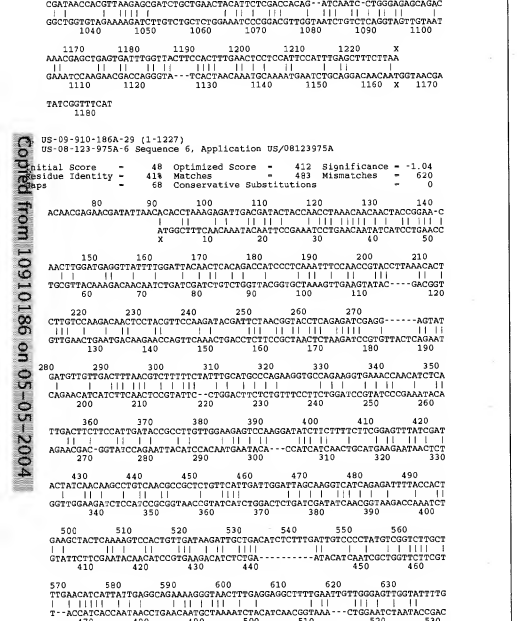


Copied from 10910186 on 05-05-2004



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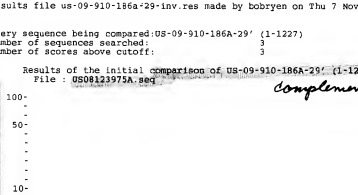
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29-inv.res made by bobryen on Thu 7 Nov 102 14:50:14-PST.

Query sequence being compared:US-09-910-186A-29' (1-1227)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

        Results of the initial comparison of US-09-910-186A-29' (1-1227) with:
          File : US08123975A.seq
```

Complement




```
                              PARAMETERS

Similarity matrix          Unitary     K-tuple                          4
Mismatch penalty                 1     Joining penalty                 30
Gap penalty                   5.00     Window size                    500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                          SEARCH STATISTICS

Scores:                       Mean        Median      Standard Deviation
                                34            33                    2.31

Times:                         CPU                     Total Elapsed
                      00:00:00.00                     00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	36 455	0.87	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	36 455	0.87	0
3. US-08-123-975A-6	Sequence 6, Application U	1351	32 372	-0.87	0

```
1. US-09-910-186A-29' (1-1227)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =      36  Optimized Score  =     455  Significance =  0.87
Residue Identity =     42%  Matches          =     549  Mismatches   =   651
Gaps             =      98  Conservative Substitutions               =     0

                          X    10        20        30        40
                TTAAGAAAGCTCAAATGGAATGGAGGAGTTCAAAGTGGA-------AGTAA
                | | | | |  ||  ||  |  |  ||  |  |  ||  |       |  ||
      CGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAA
        20        30    X   40        50        60        70        80

             50        60        70        80        90       100       110
      CCAAATCAC----TCAGCTCGTTTGTCTGCTCTCCCAGGATTGATCTGTGGTCGAGAATGTAGTTC-AGCAG
        |  |||||    ||  |  ||  |  ||  |  ||  |  ||  |  |  ||  |  |||  | |  |
      TCCAATCACCTCGAGCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCG
        90       100       110       120       130       140       150

                  120       130       140       150       160       170
      ATCGCTCTTAACGTGGT---TATCGTACTTCTTCAACTTACCAACCTTGGCCTCAT--TGATCAACTTCATC
        ||||    ||  |  |   |  |  ||  |  ||||  |  |  ||  |||  ||    |||  ||  |||
      ATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTCAAGAATGCTATC
      160       170       180       190       200       210       220       230

      180       190       200       210       220       230       240       250
      AAGTAAGAGATAGAGGATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAAC
        ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||
      GTATACAACTCTATGTGAAAAGCTCTCCACCTCCTTCGATCGTAATCGCCGAATACTCTCAACTCCATC
                240       250       260       270       280       290       300

                250       260       270       280       290       300       310       320
      TCT-TCTTCAATGTTGTTGATATTGTATTCAG-ATTCAAGTCYGTTCTTCTCATCGGAAGTATAGTTGTTGT
      |||  ||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||
      TCTCTGAACAATGAATACACCATCAACTCGATGGAAAACAATTCTGGT--TGGAAAGTATCTCTGAACT
                310       320       330       340       350       360       370

                330       340       350       360       370       380
      AC-TTGTATTCAATTGCAGTCTTGATAGCATCGACTTGGTTTGCAGAGCCTGGTA--CATTTGCTC-----
        ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |||||
      ACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
                380       390       400       410       420       430       440

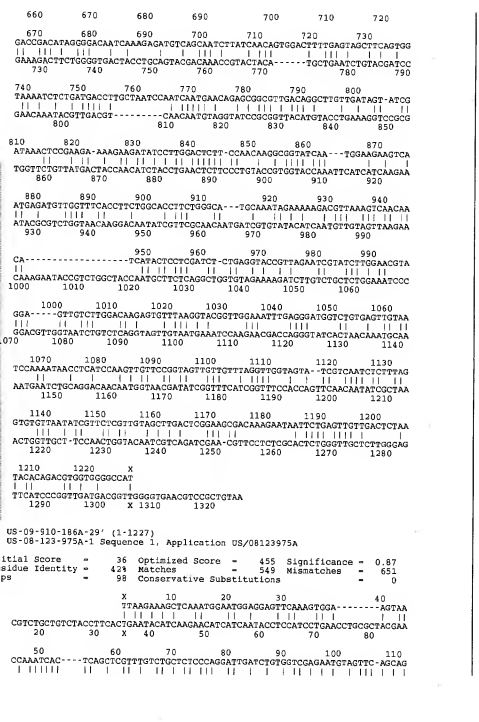
                390       400       410       420       430       440
      -------CTTTCTCTTGTTAAATTGAGTGTTAATTCTAGTAAGCCAGTTTGATACAATCCATGAGTAGAT-TT
             |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  ||
      TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
           450       460       470       480       490       500       510

      450       460       470       480       490       500       510       520
      CCTTCCACTTAGCCCTCTTTCGATCAAGGAGTTGTTAATAGCTTTAATTGCTTTATTCTTGTTCCTGTATG
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      AAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATA
        520       530       540       550       560       570       580

                530       540       550       560       570       580       590
      AATCGATGTAGGACTTGATCGTAAAACTAAAATGACAGGAATGGTAAGTTCTGGAACAAACTCCAACAAAA
      |  ||||  |  |  |  |  |  |  |  |||||  |  |  |  |  |  |  |  |  |  |  |  |
      ACATCATGTTCAAACTGGACG-----GTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCT
      590       600       610       620       630       640       650

                600       610       620       630       640       650       660
      TACCAACTCCCAACAATTCAAAAGCCTCTCAAAGTTACCCTTTTCTGCCTCAATAATGATGTTCAAAGCAA
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      GTTCGACAAAGAACTGAACGAAAAAGAAATCAAAG---ACCTGTACGACAACCAGTCCAATTCTGGTATCCT
```

Copied from 10910186 on 05-05-2004



2. US-09-910-186A-29' (1-1227)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	36	Optimized Score	= 455	Significance = 0.87
Residue Identity	=	42%	Matches	= 549	Mismatches = 651
Gaps	=	98	Conservative Substitutions	=	= 0

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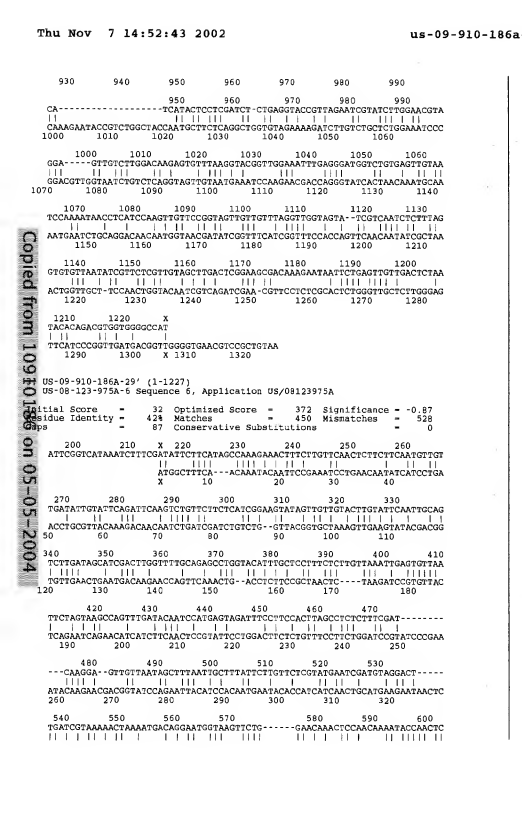

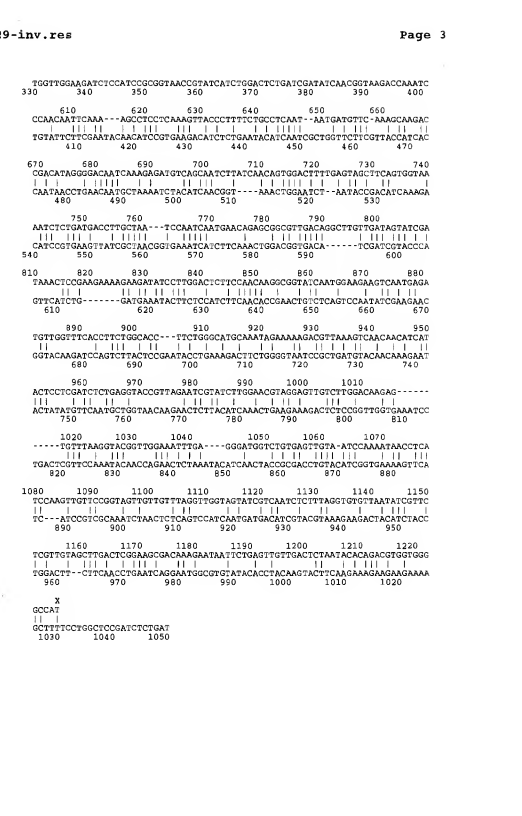

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-30.res made by bobryen on Thu 7 Nov 102 14:37:36-PST.


Query sequence being compared:US-09-910-186A-30 (1-408)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-30 (1-408) with:
        File : US08123975A.pep

 100-
    -
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  50-
    -
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    -
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    -
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  10-
    -
   5-
    -
    -
    -
    -
    -
   0-
    |    |  |    |    |    |    |    |    |    |    |    |    |
SCORE 0    19 |   38    57    76    95   114   133   152   171
STDEV         0                        1


                        PARAMETERS

Similarity matrix       PAM-150     K-tuple                     1
Threshold level of sim.     16%
Mismatch penalty             1     Joining penalty            20
Gap penalty               5.00     Window size               408
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                      SEARCH STATISTICS

Scores:                     Mean       Median    Standard Deviation
                              67           15                 89.51

Times:                       CPU                    Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                    1704
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	171	276	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	18	174	-0.55	0
3. US-08-123-975A-5	Sequence 5, Application U	439	14	134	-0.59	0

```
1. US-09-910-186A-30 (1-408)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    171  Optimized Score  =    276  Significance =  1.16
Residue Identity =    40%  Matches          =    165  Mismatches   =   202
Gaps             =      8  Conservative Substitutions               =    32

      X    10        20        30        40        50        60        70
MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTINLNNNYRNNLDEVILDYNSQTIPQISNRTLNTL
                                                                        |
                                                                        |
  APGICIDVDNEDLFPIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELLILDTDLISKIELPSENTESL
  X         10        20        30        40        50        60        70

      80        90       100       110       120       130       140
VQDNSYVPRYDSNGTSEIEETDVVDFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKD-IFFSSEFIDTI
                                                                        |
                                                                        |
TDFNVDVPYYSKQPA--IKKIPTDENTIFQYLYSQTPPLDIRDISLTSSFDDALLFSNKVYSFPSMDYIKTA
          80        90       100       110       120       130       140

     150       160       170       180       190       200       210
NKPVNAALFIDWISKVIRDFTTEATQKSFVDKIADISLIVPYVDLAINIIEAEKQNFEEAFELLGVGILLE
                                                                        |
                                                                        |
NKVVEAGLFAGWYKQIVNDFVIEANKSNTMDKIADISLIVPIYIGLALNVGNETAKGNFENAFSIAGASILLE
          150       160       170       180       190       200       210

     220       230       240       250       260       270       280
FVPELIIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWESIYSWIVSSWNLSRINTQFNKRKEQMYQA
                                                                        |
                                                                        |
PIPELLIPVVGAFLLESYID---NKNKIIKTIDNALTKRNSKWSDMYGLIVAQWLSTVNTQFYTIKEQMYKA
          220       230       240       250       260       270       280

     290       300       310       320       330       340       350
LQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKKVSLAMKNIERFMTESSISYLMKLINEAKV
                                                                        |
                                                                        |
LNYQAQALEEIIKYRYNIYSEKEKSNINIDF--NDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAV
          290       300       310       320       330       340       350

 360       370       380       390       400       X
 GKLKKYDNHVKSDLLNYILDERSILGEQINELSDLWTSFLNSSIPFELS
                                                   |
                                                   |
 EKLLDFDNYLKKNLLNYISDSNKLFLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSSIL
          360       370       380       390       400       410       420

2. US-09-910-186A-30 (1-408)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =     18  Optimized Score  =    174  Significance =  -0.55
Residue Identity =     9%  Matches          =     36  Mismatches   =   330
Gaps             =      2  Conservative Substitutions               =    26

                         X        10        20        30        40        50
                         MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTINLNNNYRNNLDEV
                                                                        |
                                                                        |
     SNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENPSTSFWIRIPKYPNSI
          10        20  X     30        40        50        60        70

          60        70        80        90       100       110       120
     ILDYNSQTIPQISNRTLNTLVDDNSYVPRYDSNGTSEIEETDVVDFNVFFYLHAQKVPEGETNISLTSSIDT
                                                                        |
                                                                        |
     SLNNEYTIINCMENNSGWKVSLNYGEIIW-TLQDTQEIKQRVFKEYSQMINISDYINRWIFVTINNRLNNS
          80        90       100       110       120       130       140
```

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   130       140       150       160       170       180       190
ALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEATQKSTVDKIADISLIVPYVGLALNIIEA
                                                                      
KIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKD
 150       160       170       180       190       200       210

  200       210       220       230       240       250       260
EKGNFEEAPELLGVGILLEFVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWKEIYSWIVSN
                                                                      
FWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKD
220       230       240       250       260       270       280       290

270       280       290       300       310       320       330       340
WLTRINTQFNKKKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKKVSLAMKNIER
                                                                      
NIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNL-SQVVVMKSKNDQGITNKCKMNLQDN
       300       310       320       330       340       350       360

       350       360       370       380       390   X   400
FMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSILGEQTNELSDLVTSTLNSSIPFELS
                                                                      
NGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEPIPVDDGWGERPL
       370       380       390       400       410   X

US-09-910-186A-30 (1-408)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     14  Optimized Score  =    134  Significance = -0.59
Residue Identity =     9%  Matches          =     29  Mismatches   =   246
Gaps             =      2  Conservative Substitutions             =    15

   100       110       120       130       140       150       160
DFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEAT
                                                                      
                FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSS
                X       10        20        30        40        50

170       180       190       200       210       220       230       240
QKSTVDKIADISLIVPYVGLALNIIEAEKGNFEEAPELLGVGILLEFVPELTIPVILVFTIKSYIDSYENK
                                                                      
ANSKIRVTQNQMIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRG--NRIIWT
       60        70        80        90       100       110       120

       250       260       270       280       290       300       310
NKAIKAINNSLIEREAKWKEIYSWIVSNWLYRINTQFNKKKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKN
                                                                      
LIDINGKTKSVFFEYNIREDISEYINRWFFVITTNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG
     130       140       150       160       170       180       190

      320       330       340       350       360       370       380
RLESEYNINNIEEELNKKVSLAMKNIERFMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSIL
                                                                      
DIDFTQFIWMKYFSIFNTELSQSNIEERIKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPV
      200       210       220       230       240       250       260

   390       400       X
GEQTNELSDLVTSTLNSSIPFELS
                        
GRILTRSKYWQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR
 270       280       290       300       310
```

Copied from 10/710,186 on 05/25/2004

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31.res made by bobryen on Thu 7 Nov 102 14:50:45-PST.

Query sequence being compared:US-09-910-186A-31 (1-1233)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

        Results of the initial comparison of US-09-910-186A-31 (1-1233) with:
            File : US08123975A.seq

 100-
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  50-
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    -
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    -
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  10-
    -
    -
   5-
    -
    -
    -
    -
    -
   0-
     |    |    |    |    |    |    |    |    |    |    |
SCORE 0    6    11   17   | 23|  |28 |   34   | 40 |  |45 |  51
SDEV          -9 -8   -7  -6  -5   -4  -3   -2 -1    0

                        PARAMETERS

Similarity matrix       Unitary     K-tuple                  4
Mismatch penalty              1     Joining penalty         30
Gap penalty                5.00     Window size            500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                  Mean        Median     Standard Deviation
                           49            46                   3.46

Times:                    CPU                     Total Elapsed
                 00:00:00.00                     00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	51	427	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	51	427	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	45	328	-1.15	0

```
1. US-09-910-186A-31 (1-1233)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   =     51  Optimized Score  =   427  Significance =  0.58
Residue Identity =   43%  Matches         =   518  Mismatches   =  599
Gaps             =    84  Conservative Substitutions =          =    0

                        X        10        20        30        40        50
                        ATGGCCAAAAATACCGGTAAATCTGAACAGTGTATTATTGTTAATAAT-GAG
                        || ||| |||| |||| |||| |||| |||| |||| |||| |||| |||
  CTAAAGTTAACTTCGATCCGATCGACAAGAAT-CAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAA
140       150       160       170       180       190       200

        60        70        80        90       100       110
  GATTTATTTTTCATAGCTA----ATAAAGATAGTTTTTCAAAAGATT---TAGCTAAAGCAGAAACTATAGC
  | | |  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||
  GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
210       220       230       240       250       260       270       280

  120       130       140       150       160       170       180
  ATATAATACACAAAAT--AATACTATAGAAAATAATTTTCTATAGATCAGTTGATTTAGATAATGAT--T
  | | |||| |||| |||  || |||| |||| |||| |||| |||| |||| |||| |||| |||  |
  CCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT
        290       300       310       320       330       340       350

      190       200       210       220       230       240       250
  TAAGCAGTGGCATAGACTTACCAAATGAAAACACAGAACCATTTACAAATTTTGACGACATAGATATCCCTG
  |||  ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||
  TGGAAAGTATCTCTGAACTAC--GGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
      360       370       380       390       400       410       420

  260       270       280       290       300       310       320
  TGTATATTAAACAACTCTGCTTTAAAAAAATTTTGTGGATGGAGATAGCCTTTTTGAAATTTACATGCTC
  |  | |||| |||  |  || ||| |||  |  || ||| |||  |  || ||| |||  |  ||| |
  TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCG-CTGGATCTCTGTTACCATCACC
      430       440       450       460       470       480       490

330       340       350       360       370       380       390
  AAACATTTCCTTCTAAATATAGAAATCTACTACAACTAAATTC----ATTAAATGATGCTTTAAGAAATAAT
  || ||  ||| |  |  | ||||||||||| | |  ||       |  | |  |  |||
  AACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACGAATCCCAATCTG
          500       510       520       530       540       550       560

  400       410       420       430       440       450
  AATAAAGTCTATACTTTT-------TTTCTACAAAC---CTTGTTGAAAAGCTAATACAGTTGTAGGTGC
  |||  || |  |||| |       | |  ||||      ||||    |  || | |  ||  |
  GGTAACATCCACGCTTCTAATAACTCATGTTCCAACTGGACGGTTGTCGTACGATCACCGCTACATCTGG
  570       580       590       600       610       620       630

460       470       480       490       500       510       520
  TTCACTTTTTGTAAACTG--GGTAAAAGGAGTAATAGATGATTTTA-CATCTGAATCCACACAAAAAAGTAC
  ||| | |  |||| |  |  |||| | |  | | |  | |  |  | |  |  |||| |  |||| |
  ATCAAATACTCCAATCTGTTCGACAAAGAACTAACGAAAAGAAATCAAGACGTGTACGACACAACCAGTCC
640       650       660       670       680       690       700       710

  530       540       550       560       570       580       590
  TATAGATAAAGTTTCAGATGTATCCATAATTATTCCCTATA-TAGGAC---CTGCTTTGAATGTAGGAAATG
  ||  |  | |  |  |  |  | |  | |  |||  |  |  |  |  | |  | |  |
  AATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACGTATCACTATGCTGAATCTG
          720       730       740       750       760       770       780

  600       610       620       630       640
  AAACAGCTAAAGAAA-------ATTTTAAAAATG----------CTTTGAAATAGGTGGA--GCCGCTAT
  |  | |  ||||       |  | |||||          ||  | |  ||  | |  |  |
```

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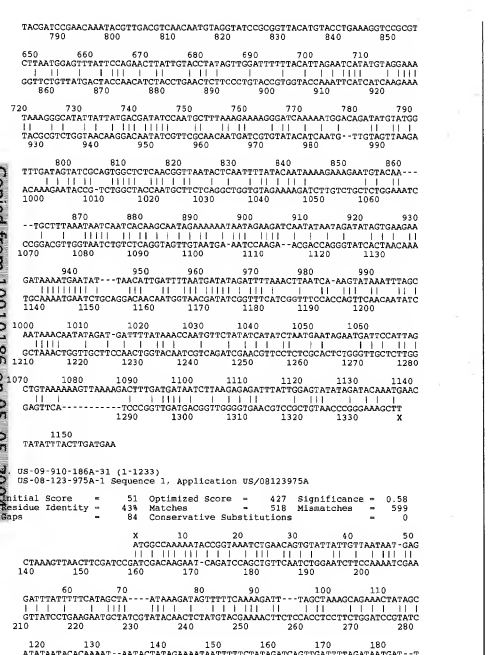
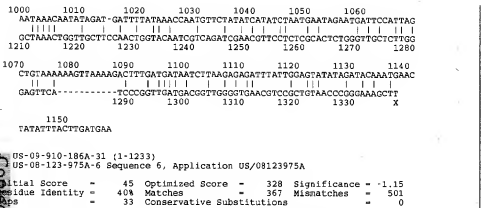


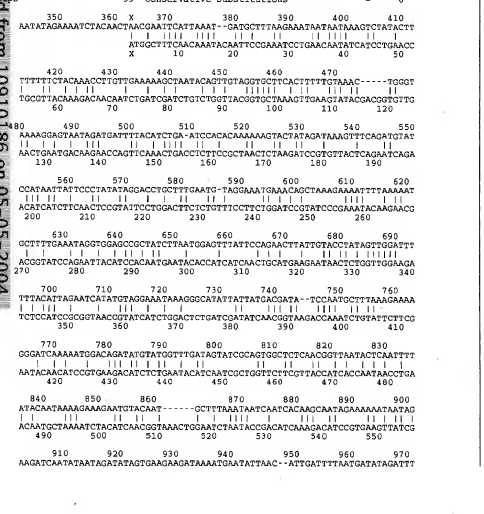
US-09-910-186A-31 (1-1233)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 51 Optimized Score = 427 Significance = 0.58
Residue Identity = 43% Matches = 518 Mismatches = 599
Gaps = 84 Conservative Substitutions = 0



US-09-910-186A-31 (1-1233)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score = 45 Optimized Score = 328 Significance = -1.15
Residue Identity = 40% Matches = 367 Mismatches = 501
Gaps = 33 Conservative Substitutions = 0



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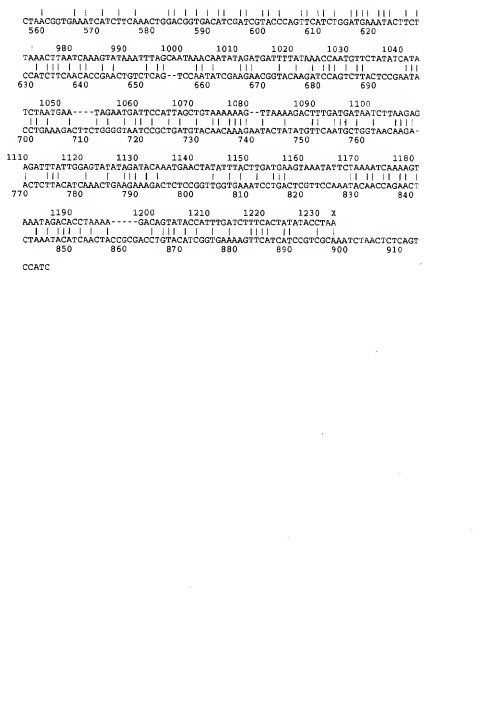

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31-inv.res made by bobryen on Thu 7 Nov 102 14:51:01-PST.

Query sequence being compared:DS-09-910-186A-31' (1-1233)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of DS-09-910-186A-31' (1-1233) with:
File : US08123975A.seq

Complement

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap Size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	44	37	7.51

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00 .

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	49	446	0.67	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	49	446	0.67	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	36	322	-1.07	0

1. US-09-910-186A-31' (1-1233)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	= 49	Optimized Score	= 446	Significance	= 0.67
Residue Identity	= 42%	Matches	= 522	Mismatches	= 640
Gaps	= 78	Conservative Substitutions			= 0

```
      20        30      X 40        50        60        70        80
AGATCAAATGGTATACTGTCTTTTAGGTGTCTATTTACTTTTGATTTTAGAATATTTACTTCATCAAGTAAA
                                                                  |||||||||
                                                                  TTCAAGTAAA
                    CTCGAGCCATGGCTCGTCTGCTG-TCTACCTTCACTGAATACATCAAGAACA
                    X         10        20        30        40        50

 90       100       110       120       130       140       150
TATAGTTCATTTGTATCTATATACTCCAATAAATCTCTCTTTAAGATTATC-ATCAAAGTCTTTTAACTTTTT
 |  |||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
TCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTAGCGTTCCA
        60        70        80        90       100       110       120

160       170       180       190       200       210       220       230
TACAGCTAATGGAATCATTCTATTCATTAGATATGATATAGAACATTGGTTTATAAAATCATCTATATTTGTT
 |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||
AAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGAT-CCAGCTGTTCAATCTGGAA
      130       140       150       160       170       180       190

 240       250       260       270       280       290       300
TATTGCTTAAATTTATACTTGCATTAAGTTTAAAATCTATATCATTAAAATCAATGTTAATATTCATTTATCC
 |||  |||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||||  |||||||
TCTTCCAAAATCGAAGTTATCCTGAAG----AATGCTATCGTATACAACTCTATGT--------ACGAAAAC
      200       210       220       230       240       250

 310       320       330       340       350       360       370
TTCTTCACTAIATACCATATAATTCATCTTCTATTATTTTTTCTATTGCTTGCTGATTGATTATTTAAAGCATT
|||| |||  |  ||  |||  | ||  ||| | | | |  | |  |||  | | |  ||
TTCTCCACCTCCTTCTGGATCCGTATCCCGAAATA---CTTCAACTCCATCTCTCTGAACAATGAATACA--
      260       270       280       290       300       310       320

 380       390       400       410       420       430       440
GTACATTCTTTCTTTCTATTGTGTCAAAATTGAGTATAACCGT---TGAGAGCCACTGCCGATACTATC-AAAC
 |||  |  |  || | | | ||||  | | | |  |  | | |||  |  |  |  |||  |  ||
--CCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGAC
            330       340       350       360       370       380       390

 450       460       470       480       490       500       510
CATACATACTGTCCATTTTTGATCCCTTTTCTTTAAAGCATTGGATATCGTCATAAATAATATGCCCTTTAT
 |  ||  |  ||  |  |  |  ||  |  |  ||  |  |  ||  |  |  ||  |  ||  |  ||
TCTGCAGGACACTCAGGAATCAAACAGCGTGTTGTATTCAAATACCTCTCAGATGAGTCAACATCTCTGACTA
      400       410       420       430       440       450       460

 520       530       540       550       560       570       580
TTCCTACATATGATTCTAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGA-----ATAAACTCCAT
 |  |  |||  ||  |  ||||| ||  |  |||||  |  |  |  |||  |  |  |||  |  |
CATCAATCGCTGGATTCTCGTTACCATCACCAACAATCGTCTGATAACTCCAAAATCTACATCAACGGCCG
      470       480       490       500       510       520       530

 590       600       610       620       630       640       650
TAAGATAGCGGCTCCACCTATTTCAAAACGATTTTAAAATTTTCTTTAGCTGTTTCATTTCCTACATTCAA
|  |||  |  |||  || ||  |  ||  || ||  |  ||  |  |  ||  |  ||  |  ||  |
TCTGATCGACCAGAAACCGATCTCCAA--TCTGGGTAACATCCAGCGT----TCTAATAACATCATGTTCA
      540       550       560       570       580       590       600

 660       670       680       690       700       710       720
AGCAGGTCCTATATAGGGAATAATATATGGATACATCTGAAACTTTATCTATAGTACTTTTTGTGTGGATTC
| | ||| |  | | | | | | | | ||||||| | |  |  ||  | |  ||  |  | | |
```

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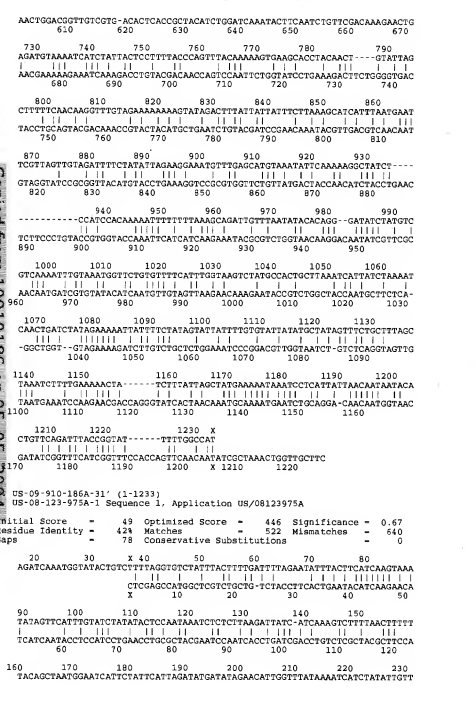

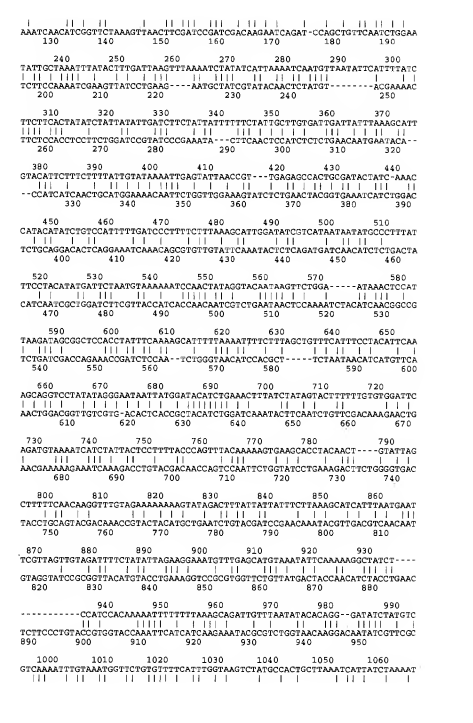

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```
  AACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACGGTCTGGCTACCAATGCTTCTCA-
960        970        980        990       1000       1010       1020       1030

   1070       1080       1090       1100       1110       1120       1130
  CAACTGATCTATAGAAAAATTATTTTCTATAGTATTATTTGTGTATTATATGCTATAGTTTCTGCTTTAGC
     |||  |   |||||||  | ||  |||    |  |  |    |  |  | ||  | |  |
  -GGCTGGT--ATAGAAAAGATCTTTGTCTGCTCTGGAAATCCGGACGTTGGTAATCT-GTCTAGGTAGTTG
          1040       1050       1060       1070       1080       1090

  1140       1150       1160       1170       1180       1190       1200
  TAAATCTTTTGAAAAACTA-------TCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACA
  |||     |  ||| |  |       |  |  |||  |||| |||  ||  |  |||||  ||
  TAATGAAATCCAAGAACGGACAGGGTATCACTAACAAATCCAAATGACTCCACAGGA-CAACAATGGTAAC
1100       1110       1120       1130       1140       1150       1160

     1210       1220       1230  X
  CTGTTCAGATTTACCGGTAT------TTTGGCCAT
     || |||  | |||| |  |      |  |||
  GATATCGGTTTCATCGGTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTC
170   1180       1190       1200      X 1210       1220

US-09-910-186A-31' (1-1233)
US-08-123-975A-6 Sequence 6, Application US/08123975A

otial Score     =     36  Optimized Score   =     322  Significance =  -1.07
ntidue Identity =    40%  Matches           =     385  Mismatches   =     492
aps             =     67  Conservative Substitutions =       0

       310        320 X      330        340        350        360        370
  TCTTCTTCACTATATCTATTATATTGATCTTCTATTATTTTTTCTATTGCTTGTGATTGATTATTTAAAGCA
     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-32.res made by bobryen on Thu 7 Nov 102 14:38:02-PST.


Query sequence being compared:US-09-910-186A-32 (1-410)
Number of sequences searched:                3
Number of scores above cutoff:               3

      Results of the initial comparison of US-09-910-186A-32 (1-410) with:
         File : US08123975A.pep

 100-
    -
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  10-
    -
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   5-
    -
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    -
    -  **                                                              *
   0+-------------------------------------------------------------------
    |    |    |    |    |    |    |    |    |    |    |    |    |    |
SCORE 0   32   63   95   126  158  189  221  252  284
STDEV       0                    1
```

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	20
Gap penalty	5.00	Window size	410
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	106	15	154.18
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	284	342	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	20	189	-0.56	0
3. US-08-123-975A-5	Sequence 5, Application U	439	14	132	-0.60	0

1. US-09-910-186A-32 (1-410)
US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score	=	284	Optimized Score	=	342
Residue Identity	=	62%	Matches	=	252
Gaps	=	1	Conservative Substitutions	=	26

Significance = 1.15
Mismatches = 125

```
          x 10        20        30        40        50        60        70
MAKNTGKSEQCIIVNNEDLPFIANKDSFSKDLAKAETIAYNIQNNTIENNFSIDQLLDNDLSSGIDLPNEN
                                                                        
          APGICIDVDNEDLPFIADKNSFSDDLSKNERIEYNYQSNYIENDFPINELLDTDLSIKIELPSEN
          X         10        20        30        40        50        60

          80        90        100       110       120       130       140
TEPPTNFDDIDIPVYIKQSALKKIFPVDGDSLFEYLHAQTPSNIENLQLTNSLNDALRNNNKVYTPFSTNLV
                                                                        
TESLTDF-NVDVPVYSEQPAIKKIFTDENTIPQYLTQSTPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
    70        80        90        100       110       120       130

          150       160       170       180       190       200       210
EKANTVVGASLFVNWVKGVIDDFTSESTQKSIIDKVSDVSIIIPYIGPALNVGNEIAKENFKNAFEIGGAAI
                                                                        
KTANKVVEAGLFAGWVKQVIVDFVTEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
140       150       160       170       180       190       200

     220       230       240       250       260       270       280
LMEPIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQVLSTVNTQFYTIKERMYNA
                                                                        
LLEPIPELLIPVVGAFLLSSYIDNKNKIIKIIDNALTRRNEKWSDMYGLIVAQVLSTVNTQFYTIKEGMYKA
210       220       230       240       250       260       270       280

     290       300       310       320       330       340       350       360
LNNGSQAIEKIIEDQYNRYSEEDKMNIIDFNDIDFKLNQSINLAINNIIDDFINQCSISYLMNNMIPLAVEK
                                                                        
LNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
          290       300       310       320       330       340       350

          370       380       390       400       410
LKDFDDNLKRDLLEYIDTNELYLLDEVNILKSKVNRHLKDSIPFDLSLYI
                                                    
LLDFDMTLKKNLLNYIDENKLYLIGSARYEKSKVNKYLKTIMPFDLSIYINDILLIEMFNKYNSEILNNI
          360       370       380       390       400  X    410       420
```

2. US-09-910-186A-32 (1-410)
US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score	=	20	Optimized Score	=	189
Residue Identity	=	10%	Matches	=	44
Gaps	=	4	Conservative Substitutions	=	29

Significance = -0.56
Mismatches = 333

```
     X         10        20        30        40        50        60        70
MAKNTGKSEQCIIVNNEDLPFIANKDSFSKDLAKAETIAYNIQNNTIENNFSIDQLLDNDLSSGIDLPNEN
                                                                        
     RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSISFWIRIPKFP
     X         10        20        30        40        50        60        70

          80        90        100       110       120       130       140
TEPPTNFDDIDIPVYIKQSALKKIFPVDGDSLFEYLHAQTPSNIENLQLTNSLNDALRNNNKVYTPFSTNLV
                                                                        
EKANTVVGASLFVNWVKGVIDDFTSESTQKSIIDKVSDVSIIIPYIGPALNVGNEIAKENFKNAFEIGGAAI
    70        80        90        100       110       120       130       140
```

```
    150       160       170       180       190       200       210
EKAMTVVGASLFVNWVKGVIDDFTSESTQKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAI
  :   : :|  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
NNSKIYINGRLIDQKPISNLGNIHASNWIMFKLDGCRDTHRYIWIKYFNLPDKELNEKEIKDLYDNQSNSGI
    150       160       170       180       190       200       210

 220       230       240       250       260       270       280
LMEPIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNA
| :|:   :   :: | | ||  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
LKDFWGDYLQYLDKPYYWLNLTEPMK---YVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKY
  220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
LNNQSQAIEKIIEDQYNRYSSEDKMNINIDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKK
  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
ASGNKDWIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPFVGNLSQVVVMKSKNDQGITNKCRM
  290       300       310       320       330       340       350

      370       380       390       400       410
LKDFDDNLKRDLLEYIDNELYLLDEVNILKSKVNRHLKDSIPFDLSLYT
  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
NLQDNNGNDIGFIGPHQFNNIAKLVASNWYNRQIERSSRTLGCSWEPIVDDGWGERPL
  360       370       380       390       400     X 410


US-09-910-186A-32 (1-410)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    14  Optimized Score  =    132  Significance = -0.60
Residue Identity =   11% Matches          =     32  Mismatches   =    239
Gaps             =     1  Conservative Substitutions =     18

       110       120       130       140       150       160       170
DSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLVEKANTVVGASLFVNWVKGVIDDFTSEST
                  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
                FNKYNSELNNILLNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSS
                X       10        20        30        40        50

      180       190       200       210       220       230       240
QKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAILMEFIPELIVPIVGFFTLESYVGNKGHI
  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
ANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI
      60        70        80        90       100       110       120

   250       260       270       280       290       300       310
IMTISNALKKRDQKWTDMYGLIVSQWLSTVNIQFYTIKERMYNALNNQSQAIEKIIEDQYNRYSEEDKMNIN
  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |  :   :  |
DINGKTKSVFFEYNIREDISEYINRWFFVTITNNLN-NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
    130       140       150       160       170       180       190

  320       330       340       350       360       370       380
IDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKKLKDFDDNLKRDLLEYIDTNELYLLDEVN
||  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
  200       210       220       230       240       250       260

390       400       X
ILKSKVNRHLKDSIPFDLSLYT
  :   :  |  :   :  |
EILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIV
270       280       290       300
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33.res made by bobryen on Thu 7 Nov 102 14:51:25-PST.


Query sequence being compared:US-09-910-186A-33 (1-1314)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-33 (1-1314) with:
          File : US08123975A.seq

 100-
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  10-
    -
    -
   5-
    -
    -
    -
    -
    -
   0-
    ----------------------------------------------------------------------
SCORE 0      62     124    |186|    248    |309|    371    | 433|    495    | 557
STDEV          -9  -8   -7   -6  -5   -4  -3   -2   -1   0


                          PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0


                        SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            533           488           40.41

Times:                       CPU                    Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Opt. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	557	788	0.59	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	557	788	0.59	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-5	Sequence 6, Application U	1351	487	678	-1.14	0

1. US-09-910-186A-33 (1-1314)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 557 Optimized Score = 788 Significance = 0.59
Residue Identity = 63% Matches = 824 Mismatches = 451
Gaps = 71 Conservative Substitutions = 0

```
           10        20        30        40        50        60
GAATTCACGATGTCTTACACTAACGACAAAATCCTGATCCTGT---ACTTCAACAAACTGTACAAAAAAATC
                                            |||   |||||||||||||||||||||||
                                            CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATC
                                            X        10        20        30        40        50

 70        80        90       100       110       120       130       140
AAAGACAACTCTATCCCTGGACATCGCTTACGAAAACAACAAATTCATCGACATCTCTGGCTATGGTTCTAAC
|||| | ||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
ATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTGCTACGCTTCCAAA
        60        70        80        90       100       110       120

          150       160       170       180       190       200       210
ATCTCTATCAAGGGTGACGTCTACATCTACTCTACTAACGCGAACCAGTTCGGTATCTACTCTTCTAAACCG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCT
  130       140       150       160       170       180       190

          220       230       240       250       260       270       280
TCTGAAGTAAACATCGCTCAGAACAACGACATCATCTACAACGGTCGTTACCAGAACTTCTCTATCTCTTTC
||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTC
200       210       220       230       240       250       260

          290       300       310       320       330       340       350
TGGGTTCGTATCCCTAAATACTTCAACAAAGTTAACCTGAACAACGAATACACTATCATCGACTGCATCCGT
||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT---G
270       280       290       300       310       320       330

 360       370       380       390       400       410       420
AACAACAACTCTGGTTGGAAATCTCTCTGAACTACAACAAAATCATCTGGACTCTGCAGGACACTGCTGGT
  | ||||| ||||||||||||| | ||||||||||||  ||||||||||||||||||||||||||||  |
 GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAA
340       350       360       370       380       390       400       410

 430       440       450       460       470       480       490       500
AACAACCAGAAACTGGTTTTCAACTACACTCAGATGATCTCTATCTCTGACTACATTAATAAATGGATCTTC
| ||| |||   | | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCAAACAGCGGTGTTGTATCCAAATACTCTCAGATGATCAACACTCTCTGACTACACTAACTCGCTGGATCTTC
          420       430       440       450       460       470       480

          510       520       530       540       550       560       570
GTTACTATCACTAACAACCGTCTGGGTAACTCTCTGTATCTACATCAACGGTAACCTGATCGATGAAAAATCT
|||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTTAGCATCACCAACAGCCGTCTGAATAACTCCAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCG
          490       500       510       520       530       540       550

          580       590       600       610       620       630       640
ATCTCTAACCTGGGTGACATCCACGTTCTGACAACATCCTGTTCAAAATCGTTGGTTGCAACGACAC---G
||||| || |||||| ||||||||||| |||| |||||||||||||||||||||| | |  ||||  |||||
ATCTCCAATCTGGGTAACATCCACGGTTCTAATAACATCATGTTCAAACTGACGGTTGTCGTGACACTCAC
          560       570       580       590       600       610       620

          650       660       670       680       690       700       710
CGTTACGTTGGTATCCGTTACTTCAAAGTTTTCGACACTGAACTGGGTAAAACTGAAATCGAAACTCTGTAC
|| ||| |  | |||  |||||||| | |||||||  ||||||  |||  |||||| ||  ||||||
```

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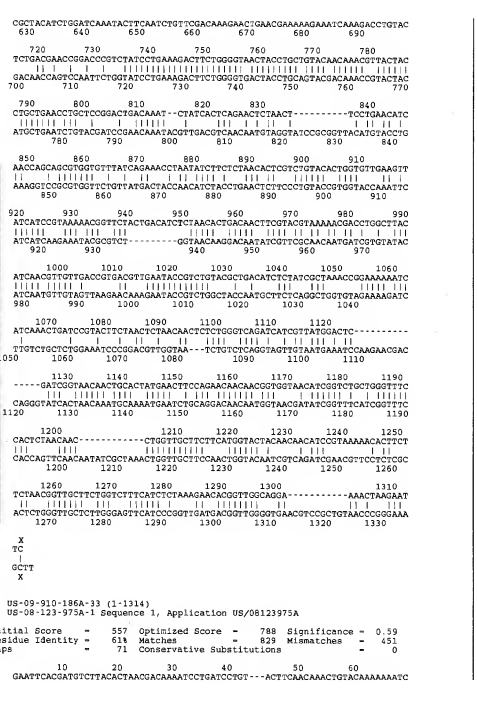

2. US-09-910-186A-33 (1-1314)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	557	Optimized Score	= 788	Significance = 0.59
Residue Identity	=	61%	Matches	= 829	Mismatches = 451
Gaps	=	71	Conservative Substitutions	=	0

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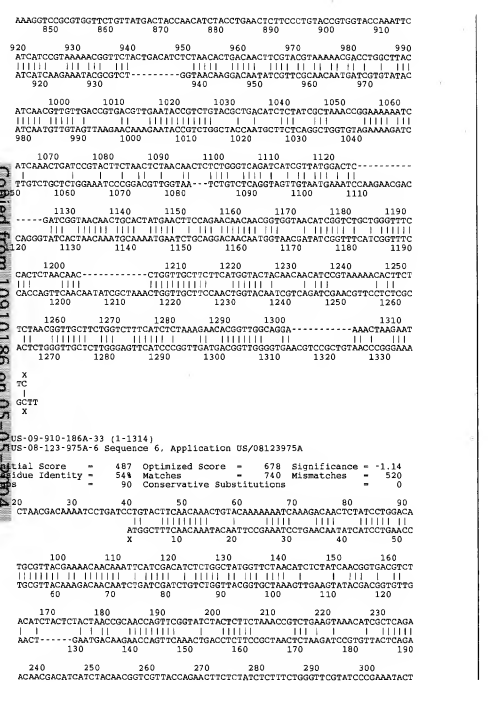

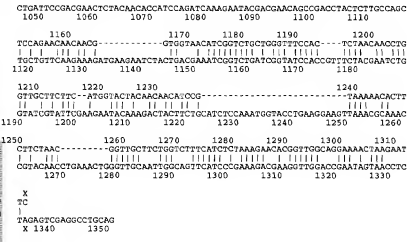

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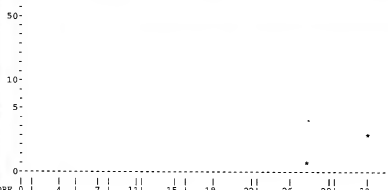
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33-inv.res made by bobryen on Thu 7 Nov 102 14:51:42-PST.

Query sequence being compared:US-09-910-186A-33' (1-1314)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-33' (1-1314) with:
File : US08123975A.seq

complement



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	31	28	3.46

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt. Score	Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	33	462	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	33	462	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	27	458	-1.15	0

1. US-09-910-186A-33' (1-1314)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	= 33	Optimized Score	= 462	Significance	= 0.58
Residue Identity	= 41%	Matches	= 560	Mismatches	= 711
Gaps	= 91	Conservative Substitutions			= 0

```
          X      10        20        30        40        50        60
          GAATTCTTAGTTTCCTGCCAACGTGTTCTTTAGAGATGAAAGACCAGAAGCAACGTTAGAAGA
          ||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACGTCCATCCTGA
          X 10        20        30        40        50        60        70

    70        80        90       100       110       120       130
AGTGTTTTACGGATGTTGTTGTAGTACCATGAAGAAGCAACCAGGTTGTTAGAGTGGAAACCCAGCA----
|||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCTGCGGCTACGAA------TCCAATCACCTGATCGACCTGTCTCG--CTACGCTTCCAAAATCAACATCGG
         80        90       100       110       120       130

   140       150       160       170       180       190       200
GACCGATGTTACCACCGTTGTTGTCTGGAAGTTCATAGTGCAGTTGTTACCGATCGAGTCCATAACGAT-G
|||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
TTCTAAAGTTAACTTCGAT-CCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCG
 140       150       160       170       180       190       200

   210       220       230       240       250       260       270
ATCTGACCCAGAGAGTTGTTAGAGTTAGAAGTACGGATCAGTTTGATGATTTTTCCGGTTTAGCGATAGAG
|||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAGTTATCCTGAAGAATGCTATCGT---ATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGA---
210       220       230       240       250       260       270

   280       290       300       310       320       330       340
ATGTCAGCGTACAGACGGTATTCAACGTCACGGTCAACAACGTTGATGTAAGCCAGGTCGTTTTACGTACG
|||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
---TCCGTATCCCGAAATACTTCAACTTCCATCTCTCTGAACAATGAATACACCATCAACTGCATGGAAA
   280       290       300       310       320       330       340

350       360       370       380       390       400       410
A-AGTTGTCAGTGTTAGAGATGTCAGTAGAACCGTTTTACGGATGATAACTTCAACAC---CAGTGTACAG
| ||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACAATTCTGGTTGGAAAGTATCTGTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCA
  350       360       370       380       390       400       410

420       430       440       450       460       470       480
ACGAGTGTTAGAGAAGATATTAGGTTTCTGATAAACACA-CGCTG-CTGGTTGATGTTCAGGAAGTTAGAG
| || ||||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
AACAGCGTGTTGTATTCAAATA-CTCTCAGATGATCAACATCTCTGACTACATCAAGCTGGATCTTCGTT
  420       430       440       450       460       470       480

490       500       510       520       530       540       550
TTCTGAGTGATAGATTTGTCAGTCCGGAGCAGGTCAGCAGGAGTAGTTTGTTTGTAC----AGCAGGTA
|  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
  490       500       510       520       530       540       550

  560       570       580       590       600       610       620
GTTACCCCAGAAGTCTTTCAGGATAGACGGGTCCGGTTCGTCAGAGTACAGAGTTTCGATTTCAGTTTACC
|||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACGC
560       570       580       590       600       610       620

  630       640       650       660       670       680       690
CAGTTCAGTGTCGAAAACTTTGAAGTAACGGATACCAACGTAACGCGTGTCGTTGCAACCAACGATTT----
|||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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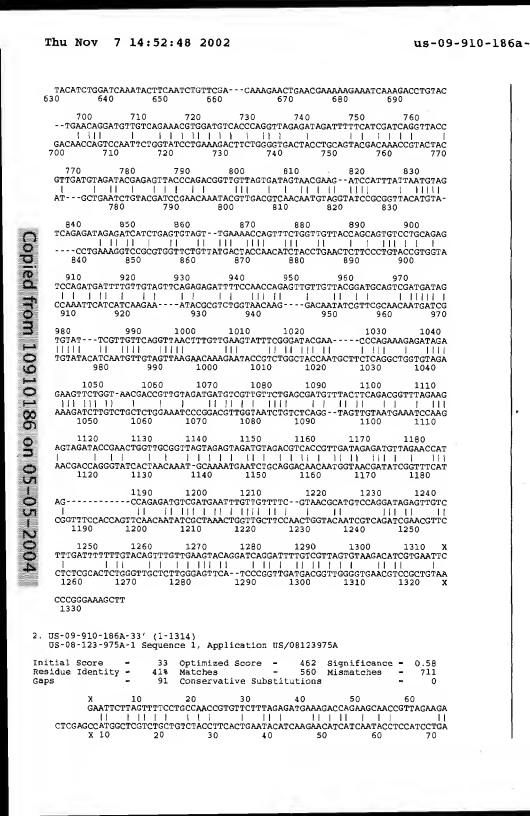

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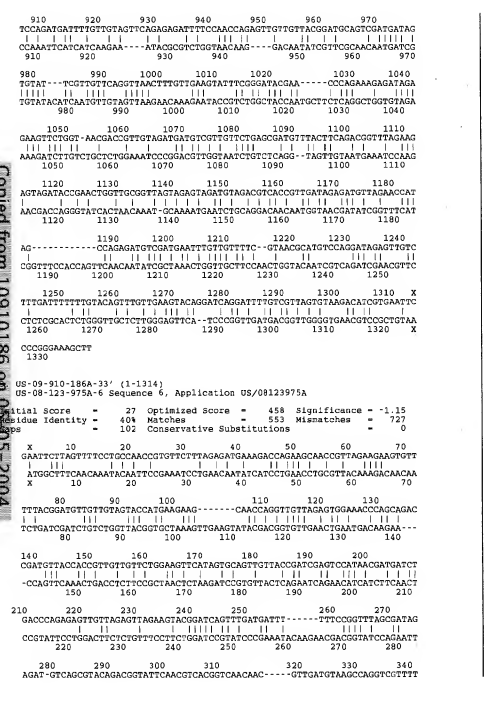

US-09-910-186A-33' (1-1314)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score	=	27	Optimized Score	= 458	Significance = -1.15
Residue Identity	=	40%	Matches	= 553	Mismatches = 727
Gaps	=	102	Conservative Substitutions		= 0

```
  TTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGT-AT
      1130       1140       1150       1160       1170       1180       1190

 1170       1180       1190       1200                  1210       1220
 AGAGATGTTAGAACCATAGCCAGAGATGTCGAT---------GAATTTGTTGTTTTCGTAACGCA---TGTC
 |   |  ||||    |      |  | |  ||              | | ||  |      |||||||    ||
 CGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCGAAACCGTA
    1200       1210       1220       1230       1240       1250       1260

 1230       1240       1250       1260       1270       1280       1290
 CAGGATAGAGTTGTCTTTGATTTTTTTGTACAGTTTGTTGAAGTACAGGATCAGGATTTTGTCGTTAGTGTA
 ||   |  |  ||  ||  | ||     || ||   |   |||  ||       |||     | || |
 CAACCTGAAACTGGGTTGCAATTGGCAGTTCA---TCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCT
   1270       1280       1290            1300       1310       1320       1330

1300       1310    X
 AGACATCGTGAATTC
 |||        |  | |
 AGAGTCGAGGCCTGCAG
    1340       1350
```

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```
> O <
O | IO  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-34.res made by bobryen on Thu 7 Nov 102 14:38:25-PST.


Query sequence being compared:US-09-910-186A-34 (1-432)
Number of sequences searched:                3
Number of scores above cutoff:               3

      Results of the initial comparison of US-09-910-186A-34 (1-432) with:
        File : USB08123975A.pep

 100-
    |
    |
  50-
    |
    |
    |
    |
    |
    |
  10-
    |
    |
   5-
    |
    |
    |
    |
   0-
    ----------------------------------------------------------------------
SCORE 0|    23 |   46 |   69 |   92 | 116 | 139 | 162 |  185 |208
STDEV -7      -6     -5     -4     -3     -2     -1     0      1


                          PARAMETERS

Similarity matrix          PAM-150     K-tuple                    1
Threshold level of sim.        16%
Mismatch penalty                1     Joining penalty           20
Gap penalty                  5.00     Window size              432
Gap size penalty             0.05
Cutoff score                    1
Randomization group             0


                       SEARCH STATISTICS

Scores:                      Mean      Median     Standard Deviation
                              181         165                  23.64

Times:                        CPU                    Total Elapsed
                      00:00:00.00                    00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Signifiance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                 Init.  Opt.
Sequence Name      Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------------
                    **** 1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U        850   208   264  1.14     0
                    **** 0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U        415   171   296 -0.42     0
  3. US-08-123-975A-5 Sequence 5, Application U        439   164   256 -0.72     0


1. US-09-910-186A-34 (1-432)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    208  Optimized Score  =    264  Significance =  1.14
Residue Identity =    35%  Matches         =    163  Mismatches   =   231
Gaps             =     28  Conservative Substitutions             =    33

                          X        10        20        30        40        50
                          MSYTNDKILILFYNKLYKKIKDNSILDMHYEYENNKFDISGYGSNISINGDVY
                          |||| ||| |||     |  | ||  :||  |  || ||||: : :   |
  AEYEKSKVWKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVE
380       390       400       410       420       430       440       450

          60        70        80        90       100       110       120
  IYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIDCIRNNNSG
     :|||   ||  | : : ||  |||:  :  ||:|||:|||| |          |||||| | : ||||
  L--NDKNQFKLTSSANSKIEVTQMQNTIFNSVFLDFSVSFWIRIPKYKNDGIQNYINHEYTIINCMK-NNSG
          460       470       480       490       500       510       520

         130       140       150       160       170       180       190
  WKISLMYNKIIWTLQDTAGNNQKLVFNYTQMISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLG
  ||||  |:|||| |           | |     ||:|||:| ||||||| | |:::|||| |       |
  WKISIRGNRIIWTLIDINGNTKSVFPEYNIREDISEYINSWFFVTITNN-LNNAKIYINGKLESNTDIKDIR
          530       540       550       560       570       580       590

         200       210       220       230       240       250       260
  DIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
  ::    | ||  | | :: :|| :|| |||     ||  |           |||||| |:||| ||: :
  EVIANSEIIFKLDGDIDRYQFIWKKYPSIFNTELSGSNIEEKYKIQSYSEYLKDFWGNPLMYNKEYYMFNAG
          600       610       620       630       640       650       660

         270       280       290       300       310       320       330
  RTDKSITQNSNF-LNIWQQRGVYQKPNIFSNTRLYIGVEVIIRKNGNSTISNTDNFVRKNDLAYINVVDRDV
     |  |  | | |  |  |  |  |  |  |  | | | |  |  |  |  |  |  |  |  |  |
  NKNSTIKLKKDSPVGEILTSKYNQNSKYINYRDLYIGEKFIIRKKSNSQSINDDIVRKEDYIYLDFFNLNQ
          670       680       690       700       710       720       730

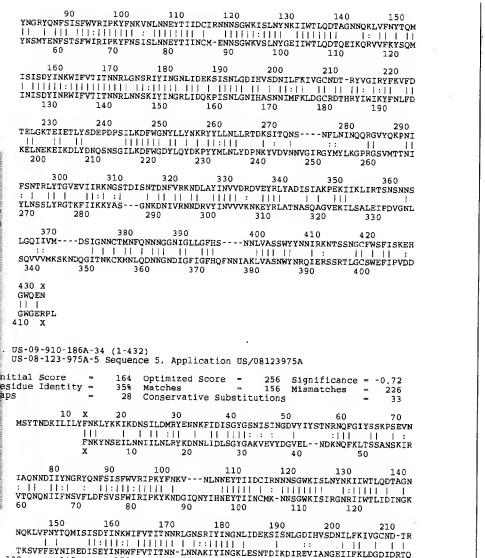
         340       350       360       370       380       390
  EYRLYADISIAKPEKIIKLLRTSNSNNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH-------
  | | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
  EWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
          740       750       760       770       780       790       800

                 400       410       420       X
  -----SNNLVASSWYYNIRKN--TSSNGCFWSFISKEHGWQEN
       |  |  |  |  |  |  |  |  |  |  |  |  |
  VPEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQPIPKDEGWTE
  810       820       830       840       850


2. US-09-910-186A-34 (1-432)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    171  Optimized Score  =    296  Significance = -0.42
Residue Identity =     49%  Matches         =    205  Mismatches   =   168
Gaps             =     17  Conservative Substitutions             =    27

    10        20        30        40        50        60        70        80
  LILYFNKLYKKIKDNSILDMRYENNKFDISGYGSNTSTNGDVYIYYSTNRNQFGIYSSKPSEVNIAQNNDII
                          |||  |  | | | |  |  |  |  |  |  |  |  |  |  |  |||
                          RTESNHLTDLSRYASKINIGSKVNFDPIDKWIQLFNLESSKIEVILKNAIV
                          X        10        20        30        40        50
```



Copied from 10910186 on 05-05-2004

US-09-910-186A-34 (1-432)
US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score = 164 Optimized Score = 256 Significance = -0.72
Residue Identity = 35% Matches = 156 Mismatches = 226
Gaps = 28 Conservative Substitutions = 33